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(54) Title: PLANT FATTY ACID SYNTHASES (57) Abstract By this invention, compositions and methods of use related to β -ketoacyl-ACP synthase, hereinafter also referred to as "synthase", are provided. Also of interest are methods and compositions of amino acid and nucleic acid sequences related to biologically active plant synthase(s) factors. Amino acid and nucleic acid for synthase protein factors are provided, as well as methods to utilize such sequences in constructs for production of genetically engineered plants having altered fatty acid compositions. In addition, uses of non-plant synthase proteins in plant genetic engineering methods are also considered.		

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PLANT FATTY ACID SYNTHASES

This application is a continuation-in-part of USSN
5 07/971,182 filed on November 2, 1992.

Field of Invention

The present invention is directed to synthase enzymes
relevant to fatty acid synthesis, amino acid and nucleic
10 acid sequences related thereto, and methods of using such
compositions in plants.

IntroductionBackground

15 Plant oils are used in a variety of industrial and
edible uses. Novel vegetable oils compositions and/or
improved means to obtain oils compositions, from
biosynthetic or natural plant sources, are needed.
Depending upon the intended oil use, various different
20 fatty acid compositions are desired.

For example, in some instances having an oilseed with
a higher ratio of oil to seed meal would be useful to
obtain a desired oil at lower cost. This would be typical
of a high value oil product. In some instances, having an
25 oilseed with a lower ratio of oil to seed meal would be
useful to lower caloric content. In other uses, edible
plant oils with a higher percentage of unsaturated fatty
acids are desired for cardio-vascular health reasons. And
alternatively, temperate substitutes for high saturate
30 tropical oils such as palm and coconut, would also find
uses in a variety of industrial and food applications.

One means postulated to obtain such oils and/or
modified fatty acid compositions is through the genetic
engineering of plants. However, in order to genetically
35 engineer plants one must have in place the means to
transfer genetic material to the plant in a stable and
heritable manner. Additionally, one must have nucleic acid
sequences capable of producing the desired phenotypic
result, regulatory regions capable of directing the correct

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application of such sequences, and the like. Moreover, it
should be appreciated that in order to produce a desired
phenotype requires that the Fatty Acid Synthetase (FAS)
pathway of the plant is modified to the extent that the
5 ratios of reactants are modulated or changed.

Higher plants appear to synthesize fatty acids via a
common metabolic pathway. In developing seeds, where fatty
acids attached to triglycerides are stored as a source of
energy for further germination, the FAS pathway is located
10 in the proplastids. The first step is the formation of
acetyl-ACP (acyl carrier protein) from acetyl-CoA and ACP
catalyzed by the enzyme, acetyl-CoA:ACP transacylase (ATA).
Elongation of acetyl-ACP to 16- and 18- carbon fatty acids
involves the cyclical action of the following sequence of
15 reactions: condensation with a two-carbon unit from
malonyl-ACP to form a β -ketoacyl-ACP (β -ketoacyl-ACP
synthase), reduction of the keto-function to an alcohol (β -
ketoacyl-ACP reductase), dehydration to form an enoyl-ACP
(β -hydroxyacyl-ACP dehydrase), and finally reduction of the
20 enoyl-ACP to form the elongated saturated acyl-ACP (enoyl-
ACP reductase). β -ketoacyl-ACP synthase I, catalyzes
elongation up to palmitoyl-ACP (C16:0), whereas β -ketoacyl-
ACP synthase II catalyzes the final elongation to stearyl-
ACP (C18:0). Common plant unsaturated fatty acids, such as
25 oleic, linoleic and α -linolenic acids found in storage
triglycerides, originate from the desaturation of stearyl-
ACP to form oleoyl-ACP (C18:1) in a reaction catalyzed by a
soluble plastid Δ -9 desaturase (also often referred to as
"stearyl-ACP desaturase"). Molecular oxygen is required
30 for desaturation in which reduced ferredoxin serves as an
electron co-donor. Additional desaturation is effected
sequentially by the actions of membrane bound Δ -12
desaturase and Δ -15 desaturase. These "desaturases" thus
create mono- or polyunsaturated fatty acids respectively.

35 A third β -ketoacyl-ACP synthase has been reported in
S. oleracea leaves having activity specific toward very
short acyl-ACPs. This acetoacyl-ACP synthase or " β -
ketoacyl-ACP" synthase III has a preference to acetyl-CoA
over acetyl-ACP, Jaworski, J.G., et al., Plant Phys. (1989)

90:41-44. It has been postulated that this enzyme may be an alternate pathway to begin FAS, instead of ATA.

Obtaining nucleic acid sequences capable of producing a phenotypic result in FAS, desaturation and/or incorporation of fatty acids into a glycerol backbone to produce an oil is subject to various obstacles including but not limited to the identification of metabolic factors of interest, choice and characterization of a protein source with useful kinetic properties, purification of the protein of interest to a level which will allow for its amino acid sequencing, utilizing amino acid sequence data to obtain a nucleic acid sequence capable of use as a probe to retrieve the desired DNA sequence, and the preparation of constructs, transformation and analysis of the resulting plants.

Thus, the identification of enzyme targets and useful plant sources for nucleic acid sequences of such enzyme targets capable of modifying fatty acid compositions are needed. Ideally an enzyme target will be amenable to one or more applications alone or in combination with other nucleic acid sequences, relating to increased/decreased oil production, the ratio of saturated to unsaturated fatty acids in the fatty acid pool, and/or to novel oils compositions as a result of the modifications to the fatty acid pool. Once enzyme target(s) are identified and qualified, quantities of protein and purification protocols are needed for sequencing. Ultimately, useful nucleic acid constructs having the necessary elements to provide a phenotypic modification and plants containing such constructs are needed.

Brief Description of the Figures

Figure 1 provides cDNA and translated amino acid sequences of a 50kD *R. communis* synthase factor B gene. Preliminary cDNA sequence and the corresponding translational peptide sequence derived from the cDNA clone, pCGN2765 (2-8), which encodes the 50kD synthase protein is shown. The cDNA includes both the postulated transit

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peptide sequence (amino acids 1-42) and the sequence
encoding the mature protein.

Figure 2 provides the *R. communis* synthase factor B 2-8
sequence with additional 3' untranslated sequence.

5 Figure 3 provides cDNA and translated amino acid
sequences of a *R. communis* 46kD synthase factor A gene.

Figures 4 and 5 provide cDNA and translated amino acid
sequences of *Brassica* synthase factor B genes.

Figure 4 provides sequences of the cDNA insert of
10 pCGN3248.

Figure 5 provides sequences of clone 4A.

Figure 6 provides cDNA sequence of a *Brassica* synthase
factor A gene. Comparison of the translated amino acid
sequence to the *R. communis* factor A sequence reveals a
15 possible frame shift mutation in the region near nucleotide
1120.

Figure 7 provides translated amino acid sequence of
nucleotides 79-1119 of the *Brassica* synthase A gene
sequence shown in Fig. 6.

20 Figure 8 provides translated amino acid sequence of
nucleotides 1127-1606 of the *Brassica* synthase A gene
sequence shown in Fig. 6.

Figure 9 provides approximately 2 kb of genomic
sequence of Bce4.

25 Figure 10 provides a cDNA sequence and the
corresponding translational peptide sequence derived from
C. tinctorius desaturase. The cDNA includes both the
plastid transit peptide sequence (amino acids 1-33) and the
sequence encoding the mature protein.

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Summary of the Invention

By this invention, compositions and methods of use
related to β -ketoacyl-ACP synthase, hereinafter also
referred to as "synthase", are provided. Also of interest
35 are methods and compositions of amino acid and nucleic acid
sequences related to biologically active plant synthase(s).
Various plant synthase factor A and B proteins are
described in WO 92/03564 which is hereby incorporated by
reference in its entirety. As is described herein,

synthase III constructs for expression in plant cells may also be used, either alone, or in conjunction with other plant synthase or fatty acid biosynthesis gene sequences to provide enhanced oil yields and/or altered compositions of plant seed oil.

Nucleic acid sequences encoding a synthase protein required for synthase activity in a host cell may be employed in nucleic acid constructs to modulate the amount of synthase activity present in the host cell. A synthase may be produced in host cells for harvest or as a means of effecting a contact between the synthase and its substrate. Host cells include prokaryotes and/or eukaryotes. Plant host cells containing recombinant constructs encoding a synthase protein, as well as plants and cells containing modified levels of synthase protein(s) are also provided. Additional nucleic acid sequences, such as those encoding transit peptides, may also be used, particularly where a full length clone for a particular synthase protein is not available or where a non-plant synthase sequence is used.

In addition, nucleic acid constructs may be designed to decrease expression of endogenous synthase in a plant cell as well. One example is the use of an anti-sense synthase sequence under the control of a promoter capable of expression in at least those plant cells which normally produce the enzyme.

Additionally, one may wish to coordinate expression of a synthase protein with the expression of other synthase proteins or other introduced sequences encoding enzymes related to fatty acid synthesis. For example, coordinated expression of synthase factor A and synthase factor B may be desirable to provide optimal synthase-II type activity in plant cells. Furthermore, coordinated expression of the synthase III gene with plant synthase proteins may also be desired. Examples of other enzymes related to fatty acid synthesis which may find use in conjunction with synthase proteins include plant thioesterases, especially medium-chain thioesterases, desaturases, especially Δ -9 desaturases, and the like. When nucleic acid constructs encoding such factors are prepared for introduction into a

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plant cell, the transcriptional initiation regions may be different from each other.

Furthermore, uses of non-plant synthase protein sequences in plant cells are considered herein. Such sequences may be used alone or in conjunction with plant synthase proteins. For example, constructs for expression of an *E. coli* synthase III protein in plant cells are described. Such constructs may be modified to provide optimal codons for expression in plant cells, as well as to provide transit peptide sequences to target the synthase protein to plastids for effect on the plant fatty acid synthesis reactions.

Detailed Description of the Invention

15 A plant synthase of this invention includes any sequence of amino acids, polypeptide, peptide fragment or other protein preparation, whether derived in whole or in part from natural or synthetic sources which demonstrates the ability to catalyze a condensation reaction between an acyl-ACP or acyl-CoA having a chain length of C₂ to C₁₆ and malonyl-ACP in a plant host cell. A plant synthase will be capable of catalyzing a synthase reaction in a plant host cell, i.e., in vivo, or in a plant cell-like environment, i.e., in vitro. Typically, a plant synthase will be derived in whole or in part from a natural plant source.

In addition, synthase from other sources such as bacteria or lower plants, may also be useful in plants and thus be considered a plant synthase in this invention. For example, the *E. coli* synthase protein encoded by the *fabB* gene is shown herein to have homology to plant synthase proteins. In *E. coli*, synthase I enzymatic activity is provided by a homodimer of the *fabB* gene product. Of particular interest is a gene for *E. coli* synthase III (*fabH*). Constructs for expression of the bacterial gene in plant cells will include fusion constructs to incorporate chloroplast transit peptide sequences, such that the *E. coli* synthase III gene product is directed to the site of fatty acid synthesis. In this manner, the overall lipid

yield may be increased by enhancing the first step in the FAS pathway.

Synthase I demonstrates preferential activity towards acyl-ACPs having shorter carbon chains, C₂-C₁₄; synthase II demonstrates preferential activity towards acyl-ACPs having longer carbon chains, C₁₄-C₁₆. Synthase III demonstrates preferential activity towards acyl-CoAs having very short carbon chains, C₂ to C₆. Other plant synthases may also find applicability by this invention, including synthase III type activities.

Synthases include modified amino acid sequences, such as sequences which have been mutated, truncated, increased and the like, as well as such sequences which are partially or wholly artificially synthesized. Synthases and nucleic acid sequences encoding synthases may be obtained by partial or homogenous purification of plant extracts, protein modeling, nucleic acid probes, antibody preparations, or sequence comparisons, for example. Once purified synthase is obtained, it may be used to obtain other plant synthases by contacting an antibody specific to *R. communis* synthase with a plant synthase under conditions conducive to the formation of an antigen:antibody immunocomplex and the recovery of plant synthase which reacts thereto. Once the nucleic acid sequence encoding a synthase is obtained, it may be employed in probes for further screening or used in genetic engineering constructs for transcription or transcription and translation in host cells, especially plant host cells.

Recombinant constructs containing a nucleic acid sequence encoding a synthase and a heterologous nucleic acid sequence of interest may be prepared. By heterologous is meant any sequence which is not naturally found joined to the synthase sequence. Hence, by definition, a sequence joined to any modified synthase is not a wild-type sequence. Other examples include a synthase from one plant source which is integrated into the genome of a different plant host.

Constructs may be designed to produce synthase in either prokaryotic or eukaryotic cells. The increased

expression of a synthase in a plant cell or decreased amount of endogenous synthase observed in a plant cell are of special interest. Moreover, in a nucleic acid construct for integration into a plant host genome, the synthase may be found in a "sense" or "anti-sense" orientation in relation to the direction of transcription. Thus, nucleic acids may encode biologically active synthases or sequences complementary to the sequence encoding a synthase to inhibit the production of endogenous plant synthase. By transcribing and translating a sense sequence in a plant host cell, the amount of synthase available to the plant FAS complex is increased. By transcribing or transcribing and translating an anti-sense sequence in a plant host cell, the amount of the synthase available to the plant FAS is decreased. Ideally, the anti-sense sequence is very highly homologous to the endogenous sequence. Other manners of decreasing the amount of synthase available to FAS may be employed, such as ribozymes or the screening of plant cells transformed with constructs containing sense sequences which in fact act to decrease synthase expression, within the scope of this invention. Other analogous methods may be applied by those of ordinary skill in the art.

Synthases may be used, alone or in combination, to catalyze the elongating condensation reactions of fatty acid synthesis depending upon the desired result. For example, rate influencing synthase activity may reside in synthase I-type, synthase II-type, synthase III-type or in a combination of these enzymes. Furthermore, synthase activities may rely on a combination of the various synthase factors as described in WO 92/03564.

Constructs which contain elements to provide the transcription and translation of a nucleic acid sequence of interest in a host cell are "expression cassettes". Depending upon the host, the regulatory regions will vary, including regions from structural genes from viruses, plasmid or chromosomal genes, or the like. For expression in prokaryotic or eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or

regulatable promoters may be employed. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli*, *B. subtilis*, *Saccharomyces cerevisiae*, including genes such as β -galactosidase, T7 polymerase, trp-lac (tac), trp E and the like.

An expression cassette for expression of synthase in a plant cell will include, in the 5' to 3' direction of transcription, a transcription and translation initiation control regulatory region (also known as a "promoter") functional in a plant cell, a nucleic acid sequence encoding a synthase, and a transcription termination region. Numerous transcription initiation regions are available which provide for a wide variety of constitutive or regulatable, e.g., inducible, transcription of the desaturase structural gene. Among transcriptional initiation regions used for plants are such regions associated with cauliflower mosaic viruses (35S, 19S), and structural genes such as for nopaline synthase or mannopine synthase or napin and ACP promoters, etc. The transcription/translation initiation regions corresponding to such structural genes are found immediately 5' upstream to the respective start codons. Thus, depending upon the intended use, different promoters may be desired.

Of special interest in this invention are the use of promoters which are capable of preferentially expressing the synthase in seed tissue, in particular, at early stages of seed oil formation. Selective modification of seed fatty acid/oils composition will reduce potential adverse effects to other plant tissues. Examples of such seed-specific promoters include the region immediately 5' upstream of a napin or seed ACP genes such as described in EP 0 255 378 (published 2/3/88), desaturase genes such as described in Thompson et al (*Proc. Nat. Acad. Sci.* (1991) 88:2578-2582), WO 92/03564 and Fig. 10 herein, or Bce-4 gene such as described in co-pending USSN 494,722, and Fig. 9 herein. Alternatively, the use of the 5' regulatory region associated with the plant synthase structural gene, i.e., the region immediately 5' upstream to a plant

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synthase structural gene and/or the transcription termination regions found immediately 3' downstream to the plant synthase structural gene, may often be desired. In general, promoters will be selected based upon their expression profile which may change given the particular application.

Sequences found in an anti-sense orientation may be found in cassettes which at least provide for transcription of the sequence encoding the synthase. By anti-sense is meant a DNA sequence in the 5' to 3' direction of transcription which encodes a sequence complementary to the sequence of interest. It is preferred that an "anti-sense synthase" be complementary to a plant synthase gene indigenous to the plant host. Any promoter capable of expression in a plant host which causes initiation of high levels of transcription in all storage tissues during seed development is sufficient. Seed specific promoters may be desired.

A DNA sequence of this invention may include genomic or cDNA sequence. A cDNA sequence may or may not contain pre-processing sequences, such as transit peptide sequences. Transit peptide sequences facilitate the delivery of the protein to a given organelle and are cleaved from the amino acid moiety upon entry into the organelle, releasing the "mature" protein (or enzyme). As synthases are part of the FAS pathway of plastid organelles, such as the chloroplast, proplastid, etc., transit peptides may be required to direct the protein(s) to substrate. A transit peptide sequence from any plastid-translocating sources may be employed, such as from ACP, especially seed ACP, small subunit of ribulose biphosphate carboxylase (RuBC), plant desaturase or from the native sequence naturally associated with the respective synthase.

The complete genomic sequence of a plant synthase may be obtained by the screening of a genomic library with a probe and isolating those sequences which hybridize thereto as described more fully below. Regulatory sequences immediately 5', transcriptional and translational initiation regions, and 3', transcriptional and

translational termination regions, to the synthase may be obtained and used with or without the synthase structural gene.

Other synthases and/or synthase nucleic sequences are obtainable from amino acid and DNA sequences provided herein. "Obtainable" refers to those plant synthases which have sufficiently similar sequence to that of the native sequence(s) of this invention to provide a biologically active synthase. One skilled in the art will readily recognize that antibody preparations, nucleic acid probes (DNA and RNA) and the like may be prepared and used to screen and recover synthases and/or synthase nucleic acid sequences from other sources. Thus, sequences which are homologously related to or derivations from either *R. communis* synthase I or II are considered obtainable from the present invention.

"Homologously related" includes those nucleic acid sequences which are identical or conservatively substituted as compared to the native sequence. Typically, a homologously related nucleic acid sequence will show at least about 60% homology, and more preferably at least about 70% homology, between the *R. communis* synthase and the given plant synthase of interest, excluding any deletions which may be present. Homology is determined upon comparison of sequence information, nucleic acid or amino acid, or through hybridization reactions.

Probes can be considerably shorter than the entire sequence, but should be at least about 10, preferably at least about 15, more preferably at least 20 or so nucleotides in length. Longer oligonucleotides are also useful, up to the full length of the gene encoding the polypeptide of interest. Both DNA and RNA can be used.

A genomic library prepared from the plant source of interest may be probed with conserved sequences from a *R. communis* synthase cDNA to identify homologously related sequences. Use of an entire *R. communis* synthase cDNA may be employed if shorter probe sequences are not identified. Positive clones are then analyzed by restriction enzyme digestion and/or sequencing. In this general manner, one

or more sequences may be identified providing both the coding region, as well as the transcriptional regulatory elements of the synthase gene from such plant source.

cDNA libraries prepared from other plant sources of interest may be screened as well, providing the coding region of synthase genes from such plant sources.

In use, probes are typically labeled in a detectable manner (for example with ^{32}P -labeled or biotinylated nucleotides) and are incubated with single-stranded DNA or RNA from the plant source in which the gene is sought, although unlabeled oligonucleotides are also useful. Hybridization is detected, typically using nitrocellulose paper or nylon membranes by means of the label after single-stranded and double-stranded (hybridized) DNA or DNA/RNA have been separated. Hybridization techniques suitable for use with oligonucleotides are well known to those skilled in the art. Thus, plant synthase genes may be isolated by various techniques from any convenient plant. Plant genes for synthases from developing seed obtained from other oilseed plants, such as *C. tinctorius* seed, rapeseed, cotton, corn, soybean cotyledons, jojoba nuts, coconut, peanuts, oil palm and the like are desired as well as from non-traditional oil sources, such as *S. oleracea* chloroplast, avocado mesocarp, *Cuphea*, California Bay and *Euglena gracillis*. Synthases, especially synthase I, obtained from *Cuphea* may show specialized activities towards medium chain fatty acids. Such synthase may be of special interest for use in conjunction with a plant medium-chain thioesterase.

Once the desired plant synthase sequence is obtained, it may be manipulated in a variety of ways. Where the sequence involves non-coding flanking regions, the flanking regions may be subjected to resection, mutagenesis, etc. Thus, transitions, transversions, deletions, and insertions may be performed on the naturally occurring sequence. In addition, all or part of the sequence may be synthesized, where one or more codons may be modified to provide for a modified amino acid sequence, or one or more codon mutations may be introduced to provide for a convenient

restriction site or other purpose involved with construction or expression. The structural gene may be further modified by employing synthetic adapters, linkers to introduce one or more convenient restriction sites, or the like. For expression, the open reading frame coding for the plant synthase or functional fragment thereof will be joined at its 5' end to a transcriptional initiation regulatory control region. In some instances, such as modulation of plant synthase via a nucleic acid sequence encoding synthase in an anti-sense orientation, a transcription initiation region or transcription/translation initiation region may be used. In embodiments wherein the expression of the synthase protein is desired in a plant host, a transcription/translation initiation regulatory region, is needed. Additionally, modified promoters, i.e., having transcription initiation regions derived from one gene source and translation initiation regions derived from a different gene source or enhanced promoters, such as double 35S CaMV promoters, may be employed for some applications.

As described above, of particular interest are those 5' upstream non-coding regions which are obtained from genes regulated during seed maturation, particularly those preferentially expressed in plant embryo tissue, such as ACP-and napin-derived transcription initiation control regions. Such regulatory regions are active during lipid accumulation and therefore offer potential for greater control and/or effectiveness to modify the production of plant desaturase and/or modification of the fatty acid composition. Especially of interest are transcription initiation regions which are preferentially expressed in seed tissue, i.e., which are undetectable in other plant parts. For this purpose, the transcript initiation region of acyl carrier protein isolated from *B. campestris* seed and designated as "Bcg 4-4" and a gene having an unknown function isolated from *B. campestris* seed and designated as "Bce-4" are also of substantial interest.

Briefly, Bce4 is found in immature embryo tissue at least as early as 11 days after anthesis (flowering),

peaking about 6 to 8 days later or 17-19 days post-anthesis, and becoming undetectable by 35 days post-anthesis. The timing of expression of the Bce4 gene closely follows that of lipid accumulation in seed tissue.

5 Bce4 is primarily detected in seed embryo tissue and to a lesser extent found in the seed coat. Bce4 has not been detected in other plant tissues tested, root, stem and leaves.

Bce4 transcript initiation regions will contain at least 1 kb and more preferably about 5 to about 7.5 kb of sequence immediately 5' to the Bce4 structural gene.

The Bcg 4-4 ACP message presents a similar expression profile to that of Bce4 and, therefore, also corresponds to lipid accumulation in the seed tissue. Bcg 4-4 is not found in the seed coat and may show some differences in expression level, as compared to Bce4, when the Bcg 4-4 5' non-coding sequence is used to regulate transcription or transcription and translation of a plant Δ -9 desaturase of this invention.

20 The napin 1-2 message is found in early seed development and thus, also offers regulatory regions which can offer preferential transcriptional regulation of a desired DNA sequence of interest such as the plant desaturase DNA sequence of this invention during lipid accumulation. Napins are one of the two classes of storage proteins synthesized in developing *Brassica* embryos (Bhatty, et al., *Can J. Biochem.* (1968) 46:1191-1197) and have been used to direct tissue-specific expression when reintroduced into the *Brassica* genome (Radke, et al., *Theor. Appl. Genet.* (1988) 75:685-694).

30 As to regulatory transcript termination regions, these may be provided by the DNA sequence encoding the plant synthase or a convenient transcription termination region derived from a different gene source, especially the transcript termination region which is naturally associated with the transcript initiation region. Typically, the transcript termination region will contain at least about 1 kb, preferably about 3 kb of sequence 3' to the structural gene from which the termination region is derived.

In developing the DNA construct, the various components of the construct or fragments thereof will normally be inserted into a convenient cloning vector which is capable of replication in a bacterial host, e.g., *E. coli*. Numerous vectors exist that have been described in the literature. After each cloning, the plasmid may be isolated and subjected to further manipulation, such as restriction, insertion of new fragments, ligation, deletion, insertion, resection, etc., so as to tailor the components of the desired sequence. Once the construct has been completed, it may then be transferred to an appropriate vector for further manipulation in accordance with the manner of transformation of the host cell.

Normally, included with the DNA construct will be a structural gene having the necessary regulatory regions for expression in a host and providing for selection of transformed cells. The gene may provide for resistance to a cytotoxic agent, e.g. antibiotic, heavy metal, toxin, etc., complementation providing prototrophy to an auxotrophic host, viral immunity or the like. Depending upon the number of different host species into which the expression construct or components thereof are introduced, one or more markers may be employed, where different conditions for selection are used for the different hosts.

The manner in which the DNA construct is introduced into the plant host is not critical to this invention. Any method which provides for efficient transformation may be employed. Various methods for plant cell transformation include the use of Ti- or Ri-plasmids, microinjection, electroporation, liposome fusion, DNA bombardment or the like. In many instances, it will be desirable to have the construct bordered on one or both sides by T-DNA, particularly having the left and right borders, more particularly the right border. This is particularly useful when the construct uses *A. tumefaciens* or *A. rhizogenes* as a mode for transformation, although the T-DNA borders may find use with other modes of transformation.

Where *Agrobacterium* is used for plant cell transformation, a vector may be used which may be

introduced into the *Agrobacterium* host for homologous recombination with T-DNA or the Ti- or Ri-plasmid present in the *Agrobacterium* host. The Ti- or Ri-plasmid containing the T-DNA for recombination may be armed (capable of causing gall formation) or disarmed (incapable of causing gall formation), either being permissible, so long as the *vir* genes are present in the transformed *Agrobacterium* host. The armed plasmid can give a mixture of normal plant cell and gall.

10 A preferred method for the use of *Agrobacterium* as the vehicle for transformation of plant cells employs a vector having a broad host range replication system, at least one T-DNA boundary and the DNA sequence or sequences of interest. Commonly used vectors include pRK2 or
15 derivatives thereof. See, for example, Ditta et al., *PNAS USA*, (1980) 77:7347-7351 and EPA 0 120 515, which are incorporated herein by reference. Normally, the vector will be free of genes coding for opines, oncogenes and *vir*-genes. Included with the expression construct and the T-
20 DNA will be one or more markers, which allow for selection of transformed *Agrobacterium* and transformed plant cells. A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. The
25 particular marker employed is not essential to this invention, one or another marker being preferred depending on the particular host and the manner of construction.

The vector is used for introducing the DNA of interest into a plant cell by transformation into an *Agrobacterium*
30 having *vir*-genes functional for transferring T-DNA into a plant cell. The *Agrobacterium* containing the broad host range vector construct is then used to infect plant cells under appropriate conditions for transfer of the desired DNA into the plant host cell under conditions where
35 replication and normal expression will occur. This will also usually include transfer of the marker, so that cells containing the desired DNA may be readily selected.

The expression constructs may be employed with a wide variety of plant life, particularly plant life involved in

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the production of vegetable oils. These plants include, but are not limited to rapeseed, peanut, sunflower, *C. tinctorius*, cotton, *Cuphea*, soybean, and corn or palm.

For transformation of plant cells using *Agrobacterium*, explants may be combined and incubated with the transformed *Agrobacterium* for sufficient time for transformation, the bacteria killed, and the plant cells cultured in an appropriate selective medium. Once callus forms, shoot formation can be encouraged by employing the appropriate plant hormones in accordance with known methods and the shoots transferred to rooting medium for regeneration of plants. The plants may then be grown to seed and the seed used to establish repetitive generations and for isolation of vegetable oils.

The invention now being generally described, it will be more readily understood by reference to the following examples which are included for purposes of illustration only and are not intended to limit the present invention.

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EXAMPLES

Example 1. Analysis of Synthase Proteins

In purification of synthase proteins as discussed in WO 92/03564, synthase II activity was observed only when both the 46 and 50kD peptides were present in *R. communis* protein preparations, while synthase I activity was detected in preparations containing only the 50kD peptide. In addition, *E. coli* expression data demonstrated that both the 46kD and 50kD synthase factors (factors A and B, respectively) were required for synthase II type activity, and that synthase factor A contributes the longer chain fatty acyl substrate specificity to synthase II activity.

To determine whether synthase II activity requires two discrete proteins or a single heterodimer, covalent intramolecular bonds are introduced into the purified protein preparation and the products of this reaction identified by SDS-PAGE and Western analysis. A similar analysis is conducted with a synthase I preparation to determine if synthase I activity is provided by a single peptide, or a homodimer of the observed 50kD peptide.

Twenty μ g (400pmol of 46kD and 50kD peptides) of a purified synthase II preparation in "20 buffer", is combined with 40nmol of EGS (ethylene glycol bis(succinimidyl succinate)) in 10% Me₂SO, to a final volume of 0.4ml. The reaction is stopped by addition of 0.045ml of 2M Tris-HCl, pH 7.0, and the protein is prepared immediately for gel electrophoresis by the addition of SDS-PAGE sample buffer containing β -mercaptoethanol. A purified preparation of synthase I is similarly treated, except that 600ng (12pmol of 50kD peptide) is combined with 8.3nmol of EGS in a volume of 85 μ l. This reaction is stopped by addition of 9 μ l of 2M Tris-HCl, pH 7.0. The crosslinked proteins are analyzed by SDS-PAGE, Western transfer and antibody blotting.

Each of the two active sites on a molecule of EGS can form a covalent bond with any available amino group of the studied proteins, resulting in linkage of the two amino groups across an EGS bridge. With synthase II, at room temperature incubations of 10 or 30 minutes in from 0.1mM to 10mM EGS, only two major and two minor species of crosslinked proteins are formed. These proteins are observed to migrate on SDS-PAGE at about 124 and 107kD, suggesting that the proteins are dimers. By Western analysis, all crosslinked products react positively with antibodies raised against both the 46 and 50kD peptides, indicating that both peptides are present in all products of crosslinking. The appearance of more than one dimer could reflect different conformations of the dimers depending on the number and the locations of intramolecular bond formations. Only after prolonged incubation, or with higher concentrations of EGS, are multimeric protein species formed. These results provide additional evidence that the synthase II protein is a heterodimer of the 46 and 50kD subunits.

When synthase I protein is subjected to the same reactions, one major and two minor products are formed, each of which has a mobility of about 116kD. All three of these products react with antibody raised against the 50kD

peptide, but not with antibodies raised against the 46kD peptide. These results suggest that the protein having synthase I activity is a homodimer of the 50kD peptide.

5 **Example 2. Synthase Gene Sequence**

The preparation of a cDNA libraries, using the methods as described in Alexander, et al. (*Methods in Enzymology* (1987) 154:41-64), and the screening of the cDNA libraries for synthase cDNA clones are described in WO 92/03564.

10 Sequences of plant synthase factor proteins A and B which have been shown to be required for synthase II activity are provided herein in Figures 1-8. It is noted that synthase factor B protein is also required for plant synthase I type activity (WO 92/03564)

15 Sequence of an *E. coli* synthase III gene is found in Tsay et. al. (*J. Biol. Chem.* (1992) 267:6807-6814)

Example 3. Expression Cassettes

In this example, expression cassettes suitable for
20 insertion of synthase genes are described.

Expression cassettes utilizing 5'-upstream sequences and 3'-downstream sequences of genes preferentially expressed during seed development can be constructed from isolated DNA sequences of genes with an appropriate
25 expression pattern. Examples of genes which are expressed during seed development in *Brassica* are a napin gene, 1-2, and an ACP gene, Bcg4-4, both described in European Patent Publication EP 0 255 378, and a Bce4 gene, as described below. The napin gene encodes a seed storage protein that
30 is preferentially expressed in immature embryos which are actively producing storage proteins. The ACP gene encodes a protein which is an integral factor in the synthesis of fatty acids in the developing embryo and is preferentially expressed during fatty acid synthesis. Bce4 is a gene that
35 produces a protein of unknown function that is preferentially expressed early in embryo development, at about 15-19 days post-anthesis, and is also detectable as early as 11 days post-anthesis. The sequence of Bce4 is shown in Figure 9.

DNA sequences that control the expression of these genes can be isolated and sufficient portions of the 5' and 3' regulatory regions combined such that a synthase gene inserted between these sequences will be preferentially expressed early in seed development. This expression pattern will allow the synthase gene to affect fatty acid synthesis, which also occurs early in seed development. For example, a 1.45 kb *XhoI* fragment containing 5' sequence and a 1.5 kb *SstI/BglIII* fragment containing 3' sequence of the Bcg4-4 ACP gene can be combined in an ACP expression cassette using a variety of available DNA manipulation techniques. Similarly, a napin expression cassette can be prepared that contains approximately 1.725 kb of 5' sequence from an *EcoRV* site to immediately before the ATG start codon and approximately 1.25 kb of 3' sequence from an *XhoI* site approximately 18 bases past the TAG stop codon to a 3' *HindIII* site of a 1-2 napin gene. A Bce4 expression cassette can be made by combining approximately 7.4 kb of 5' DNA sequence from an upstream *PstI* site to immediately before the ATG start codon with approximately 1.9 kb of 3' sequences from immediately after the TAA stop codon to a 3' *PstI* site.

Variations can be made in these expression cassettes such as increasing or decreasing the amounts of 5' and 3' sequences, combining the 5' sequences of one gene with the 3' sequences of a different gene (for example using the 1.3 kb 5' sequences of napin 1-2 with the 1.5 kb 3' sequences of ACP Bcg4-4 in an expression cassette), or using other available 3' regulatory sequences, as long as these variations result in expression cassettes that allow for expression of the inserted synthase gene at an appropriate time during seed development.

A. Napin Seed Specific Expression Cassettes

1. Napin 1-2 pCGN1808 Expression Cassette

An expression cassette utilizing 5' upstream sequences and 3' downstream sequences obtainable from *B. campestris* napin gene can be constructed as follows.

A 2.7 kb *XhoI* fragment of napin 1-2 (See, Figure 2 of EP 0 255 378, published February 3, 1988) containing 5'

upstream sequences is subcloned into pCGN789 (a pUC based vector with the normal polylinker replaced by the synthetic linker which encodes the restriction digestion sites *EcoRI*, *SallI*, *BglIII*, *PstI*, *XhoI*, *BamHI*, *HindIII*) and results in pCGN940. The majority of the napin coding region of pCGN940 was deleted by digestion with *SallI* and religation to form pCGN1800. Single-stranded DNA from pCGN1800 was used in an in vitro mutagenesis reaction (Adelman et al., DNA (1983) 2:183-193) using a synthetic oligonucleotide which inserted *EcoRV* and *NcoI* restriction site at the junction of the promoter region and the ATG start codon of the napin gene. An appropriate mutant was identified by hybridization to the oligonucleotide used for the mutagenesis and sequence analysis and named pCGN1801.

A 1.7 kb promoter fragment was subcloned from pCGN1801 by partial digestion with *EcoRV* and ligation to pCGN786 (a pCGN566 (polylinker in opposite orientation as pCGN565 described in WO 92/03564) chloramphenicol based vector with the synthetic linker described above in place of the normal polylinker) cut with *EcoRI* and blunted by filling in with DNA Polymerase I Klenow fragment to create pCGN1802.

A 2.1 kb *SallI* fragment of napin 1-2 containing 3' downstream sequences is subcloned into pCGN789 (described above) and results in pCGN941. pCGN941 is digested with *XhoI* and *HindIII* and the resulting approximately 1.6 kb of napin 3' sequences are inserted into *XhoI-HindIII* digested pCGN1802 to result in pCGN1803. In order to remove a 326 nucleotide *HindIII* fragment inserted opposite to its natural orientation, as a result of the fact that there are 2 *HindIII* sites in pCGN1803, the pCGN1803 is digested with *HindIII* and religated. Following religation, a clone is selected which now contains only 1.25 kb of the original 1.6 napin 3' sequence. This clone, pCGN1808 is the napin 1-2 expression cassette and contains 1.725 kb of napin promoter sequences and 1.265 kb of napin 3' sequence with the unique cloning sites *SallI*, *BglII*, *PstI* and *XhoI* in between.

2. Napin 1-2 pCGN3223 Expression Cassette

Alternatively, pCGN1808 may be modified to contain flanking restriction sites to allow movement of only the expression sequences and not the antibiotic resistance marker to binary vectors such as pCGN1557 (McBride and Summerfelt, *supra*). Synthetic oligonucleotides containing KpnI, NotI and HindIII restriction sites are annealed and ligated at the unique HindIII site of pCGN1808, such that only one HindIII site is recovered. The resulting plasmid, pCGN3200 contains unique HindIII, NotI and KpnI restriction sites at the 3'-end of the napin 3'-regulatory sequences as confirmed by sequence analysis.

The majority of the napin expression cassette is subcloned from pCGN3200 by digestion with HindIII and SacI and ligation to HindIII and SacI digested pIC19R (Marsh, et al. (1984) *Gene* 32:481-485) to make pCGN3212. The extreme 5'-sequences of the napin promoter region are reconstructed by PCR using pCGN3200 as a template and two primers flanking the SacI site and the junction of the napin 5'-promoter and the pUC backbone of pCGN3200 from the pCGN1808 construct. The forward primer contains ClaI, HindIII, NotI, and KpnI restriction sites as well as nucleotides 408-423 of the napin 5'-sequence (from the EcoRV site) and the reverse primer contains the complement to napin sequences 718-739 which include the unique SacI site in the 5'-promoter. The PCR was performed using a Perkin Elmer/Cetus thermocycler according to manufacturer's specifications. The PCR fragment is subcloned as a blunt-ended fragment into pUC8 (Vieira and Messing (1982) *Gene* 19:259-268) and digested with HincII to give pCGN3217. Sequence of pCGN3217 across the napin insert verifies that no improper nucleotides were introduced by PCR. The napin 5'-sequences in pCGN3217 are ligated to the remainder of the napin expression cassette by digestion with ClaI and SacI and ligation to pCGN3212 digested with ClaI and SacI. The resulting expression cassette pCGN3221, is digested with HindIII and the napin expression sequences are gel purified away and ligated to pIC20H (Marsh, *supra*) digested with HindIII. The final expression cassette is pCGN3223, which contains in an ampicillin resistant background, essentially

identical 1.725 napin 5' and 1.265 3' regulatory sequences as found in pCGN1808. The regulatory regions are flanked with *HindIII*, *NotI* and *KpnI* restriction sites and unique *SallI*, *BglIII*, *PstI*, and *XhoI* cloning sites are located
5 between the 5' and 3' noncoding regions.

B. Bce4 Expression Cassette

An expression cassette for seed specific expression can also be constructed from Bce4 gene sequences, such as those represented in Figure 9. Genomic clones having
10 regulatory sequences of the Bce4 gene may be isolated from a *Brassica campestris* genomic library using Bce4 sequences as probe. For example, an approximately 20 kb *BamHI* fragment is isolated and designated as clone P1C1. The approximately 20 kb insert of clone P1C1 is released by
15 *BamHI* digestion and inserted into the *BamHI* site of the binary vector pCGN1547 (see below), producing pCGN1853. The *PstI* fragment of pCGN1853, containing the Bce4 gene, is inserted into the *PstI* site of pUC18 (Norrander, et al. (1983) *Gene* 26:101-106), producing pCGN1857. The plasmid
20 pCGN1857 was deposited with the ATCC, Rockville, MD on March 9, 1990, accession number 68251. The *ClaI* fragment of pCGN1857, containing the Bce4 gene is ligated into *ClaI* digested Bluescript KS+ (Stratagene; La Jolla, CA), producing pCGN1864. Single stranded DNA is made from
25 pCGN1864 and altered by *in vitro* mutagenesis as described by Adelman et al. (*DNA* (1983) 2:183-193) using oligonucleotides having homology to Bce4 sequences 5' and 3' of the translated start and stop codons and also coding for restriction digest sites. The resulting plasmid,
30 pCGN1866, contains *XhoI* and *BamHI* sites (from BCE45P) immediately 5' to the Bce4 start codon and *BamHI* and *SmaI* sites (from BCE43P) immediately 3' to the Bce4 stop codon. The *ClaI* fragment of pCGN1866, containing the mutagenized sequences, is inserted into the *ClaI* site of pCGN2016
35 (described below), producing pCGN1866C. The *ClaI* fragment of pCGN1866C is used to replace the corresponding wild-type *ClaI* fragment of pCGN1867 (described below) to produce pCGN1868. Bce4 coding sequences are removed by digestion of pCGN1868 with *BamHI* and recircularization of the plasmid

to produce pCGN1870. The Bce4 expression cassette, pCGN1870, contains 7.4 kb of 5' regulatory sequence and 1.9 kb of 3' regulatory sequence derived from the Bce4 genomic clone separated by the cloning sites, *XhoI*, *BamHI*, and *SmaI*.

pCGN1867

The *BamHI* and *SmaI* sites of pUC18 (Norrande et al., (1983) supra) are removed by *BamHI*-*SmaI* digestion and recircularization of the plasmid, without repair of the ends, to produce pCGN1862. The *PstI* fragment of pCGN1857, containing the Bce4 gene, is inserted into the *PstI* site of pCGN1862 to produce pCGN1867.

pCGN2016

The multiple cloning sites of pUC12-Cm (Buckley, K., Ph.D. Thesis, UCSD, CA (1985)) are replaced by those of pUC18 to produce pCGN565. The *HhaI* fragment of pCGN565, containing the chloramphenicol resistance gene is excised, blunted by use of mung bean nuclease, and inserted into the *EcoRV* site of Bluescript KS- (Stratagene; La Jolla, CA) to create pCGN2008. The chloramphenicol resistance gene of pCGN2008 is removed by *EcoRI*-*HindIII* digestion. After treatment with Klenow enzyme to blunt the ends, the fragment carrying the chloramphenicol resistance gene is inserted into the *DraI* site of Bluescript KS-, replacing the ampicillin resistance gene of Bluescript KS-, to produce pCGN2016.

C. ACP Expression Cassette

An expression cassette utilizing 5'-upstream sequences and 3'-downstream sequences obtainable from *B. campestris* ACP gene can be constructed as follows. A 1.45kb *XhoI* fragment of Bcg 4-4 containing 5'-upstream sequences is subcloned into the cloning/sequencing vector Bluescript+ (Stratagene Cloning Systems, San Diego, CA). The resulting construct, pCGN1941, is digested with *XhoI* and ligated to a chloramphenicol resistant Bluescript M13+ vector, pCGN2015 digested with *XhoI*. pCGN2015 is described in WO 92/05364. This alters the antibiotic resistance of the plasmid from penicillin resistance to chloramphenicol resistance. The chloramphenicol resistant plasmid is pCGN1953.

3'-sequences of Bcg 4-4 are contained on an *Sst*I/*Bgl*II
fragment cloned in the *Sst*I/*Bam*HI sites of M13 Bluescript+
vector. This plasmid is named pCGN1940. pCGN1940 is
modified by in vitro site-directed mutagenesis (Adelman et
5 al., *DNA* (1983) 2:183-193) using the synthetic
oligonucleotide (SEQ ID NO:51) 5'-
CTTAAGAAGTAACCCGGGCTGCAGTTTTAGTATTAAGAG-3' to insert *Sma*I
and *Pst*I restriction sites immediately following the stop
codon of the reading frame for the ACP gene 18 nucleotides
10 from the *Sst*I site. The 3'-noncoding sequences from this
modified plasmid, pCGN1950, are moved as a *Ps*I-*Sma*I
fragment into pCGN1953 cut with *Pst*I and *Sma*I. The
resulting plasmid pCGN1977 comprises the ACP expression
cassette with the unique restriction sites *Eco*RV, *Eco*RI and
15 *Pst*I available between the 1.45kb 5' and 1.5 kb of 3'-
noncoding sequences for the cloning of genes to be
expressed under regulation of these ACP gene regions.

Example 4. Synthase Constructs

20 A. Preparation of Plant Transformation Vectors

Synthase cDNA sequences can be inserted in expression
cassettes containing plant regulatory regions using a
variety of DNA manipulation techniques. In this manner,
synthase constructs in either the sense or anti-sense
25 orientation are prepared. If convenient restriction sites
are present in the synthase clones, they may be inserted
into the expression cassette by digesting with the
restriction endonucleases and ligation into the cassette
that has been digested at one or more of the available
30 cloning sites. If convenient restriction sites are not
available in the clones, the DNA of either the cassette or
the synthase gene(s), can be modified in a variety of ways
to facilitate cloning of the synthase gene(s) into the
cassette. Examples of methods to modify the DNA include by
35 PCR, synthetic linker or adaptor ligation, in vitro site-
directed mutagenesis (Adelman et al., supra), filling in or
cutting back of overhanging 5' or 3' ends, and the like.
These and other methods of manipulating DNA are well known
to those of ordinary skill in the art.

The fragment containing the synthase gene in the expression cassette, 5' sequences/synthase/3' sequences, is then cloned into a binary vector, such as described by McBride and Summerfelt (*Pl.Mol.Biol.* (1990) 14:269-276), for *Agrobacterium* transformation. Other binary vectors are known in the art and may also be used for synthase cassettes. The binary vector containing the expression cassette and the synthase gene is transformed into *Agrobacterium tumefaciens*, such as strain EHA101 (Hood, et al., *J. Bacteriol.* (1986) 168:1291-1301) as per the method of Holsters, et al., (*Mol. Gen. Genet.* (1978) 163:181-187), and used to generate transformed plants as described in Example 5.

B. Synthase Factor A Constructs

1. Sense orientation

Constructs containing sense synthase sequences under the control of plant regulatory regions for expression in plant cells may be prepared as follows. The *R. communis* synthase factor A cDNA, 1-1A, is altered by in vitro mutagenesis to insert a *Bam*HI restriction site at the 5' end of the cDNA insert and *Xho*I and *Sma*I sites immediately 3' of the translation stop codon. The resulting construct, pCGN2781, is digested with *Bam*HI and *Xho*I and ligated into *Bgl*III and *Xho*I digested pCGN3223, the above described napin expression cassette, resulting in pCGN2785. The napin/factor A/napin region of pCGN2785 is obtained by digestion with *Asp*718 and ligated into *Asp*718 digested pCGN1557 (McBride et al.; *supra*), resulting in pCGN2787.

2. Antisense Orientation.

For antisense synthase A, a *Bam*HI/*Eco*RV fragment of the *B. campestris* synthase factor A cDNA clone, pCGN4300 (nucleotides 218-1535), is treated to create blunt ends, and subcloned into the *Eco*RV site of the ACP expression cassette, pCGN1977, to create pCGN4304. A *Kpn*I/*Xba*I fragment containing the ACP 5'/antisense Brassica factor A/ACP 3' fragment is inserted into *Kpn*I/*Xba*I digested binary vector pCGN1557 (McBride and Summerfelt, *supra*) resulting in plant transformation construct pCGN4306.

To insert the *Brassica* synthase factor A cDNA clone into a napin cassette, the *Bam*HI/*Eco*RV fragment of pCGN4300 (nucleotides 218-1535) is blunted and ligated into the *Bgl*III-digested napin cassette, pCGN3223, which has been similarly treated to provide a blunt ended DNA molecule. The resulting plasmid is pCGN4305. An Asp718 fragment containing the napin 5'/antisense *Brassica* A/napin 3' fragment is subcloned into binary vector pCGN1557 to produce a construct for plant transformation, pCGN4324.

10 3. Transit Fusion Constructs.

Due to the possibility that the *R. communis* factor A cDNA clone does not encode the entire transit peptide, DNA constructs are prepared to fuse the transit peptide encoding region from the *Brassica* factor A cDNA clone (including the V-A-A-C-M-S conserved region) to the mature peptide encoding region from the *R. communis* factor A clone. The constructs are designed such that the encoding region for the transit peptide and first 24 amino acids of the mature *R. communis* protein (lysine residue at nucleotides 365-367 of sequence shown in Figure 3 is the presumed N-terminus) is replaced with the corresponding region from the *Brassica* clone.

Two different 5' regions of the *Brassica* factor A cDNA are obtained by PCR. The "short" version includes nucleotides 79-423 of the sequence provided in Figure 6. This region encodes from the first methionine residue of the *Brassica* factor A cDNA to the histidine residue at position 115. The "long" version includes nucleotides 7-423 of the sequence shown in Figure 6, and thus includes a portion of the factor A 5' untranslated region. Each of these *Brassica* synthase factor A fragments also contains *Sal*I and *Eco*RV restriction sites at their 5' and 3' ends, respectively, which were provided in the oligonucleotide primers used in the PCR. The insertion of the 3' *Eco*RV site alters the codon for the 116 Asp from "GAC" to "GAT".

An *R. communis* synthase factor A DNA fragment, containing the encoding region for amino acids 145-540 of the sequence shown in Figure 3, and a stop codon, is also obtained by PCR. The coding sequence "GATATC" is chosen

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for the Asp and Ile amino acids at positions 145-146 in order to provide an EcoRV site at the 5' end of this fragment. The PCR primers are designed such that an XhoI site is inserted at the 3' end of this fragment immediately following the "TGA" stop codon.

The Brassica and *R. communis* synthase factor A fragments are fused by ligation of their respective 3' and 5' EcoRV sites. The fusion fragment is obtained by digestion with SalI and XhoI and ligated into the napin expression cassette, pCGN3223. The construct containing the "short" Brassica factor A is designated pCGN4313, and the construct containing the "long" Brassica factor A is designated pCGN4314. The KpnI fragments containing the napin 5'/synthase A fusion/napin 3' fragments are subcloned into binary vector pCGN1557 to produce vectors for plant transformation. The "short" Brassica factor A construct is designated pCGN4319, and the "long" Brassica factor A construct is designated pCGN4320.

A third fusion construct with the mature *R. communis* synthase factor A is prepared which incorporates the transit peptide encoding sequence of the *C. tinctorius* desaturase shown in Figure 10. A DNA fragment encoding amino acids 121-540 of Figure 3 (the mature *R. communis* synthase factor A and the asparagine residue immediately N-terminal to the mature peptide) is obtained by PCR. In addition, the sequence, CCATGGCC is included in the forward oligonucleotide primer and added at the 5' terminus of this fragment, such that an NcoI restriction site precedes the synthase sequence, and methionine and alanine residues are added to the synthase peptide encoding region. An XhoI restriction site is provided immediately following the stop codon at the 3' terminus.

The *C. tinctorius* desaturase cDNA clone shown in Figure 10, pCGN2754, is modified by PCR to insert PstI, SmaI and XhoI sites to flank the coding region. The PCR product is digested with PstI and ligated to pUC8 (Vieira and Messing (1982) Gene 19:2359-268) digested with PstI to produce pCGN3220. The large NcoI/SacI fragment of pCGN3220 containing the pUC8 vector and the *C. tinctorius* desaturase

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cdna sequence 5' to the *Nco*I site and 3' to the *Sac*I site is gel purified and ligated to the gel-purified *Nco*I/*Sac*I internal fragment of pCGN2754 resulting in pCGN3222. The coding region of the *C. tinctorius* desaturase from pCGN3222 is cloned into the pCGN3223 napin cassette by digestion with *Xho*I and ligation to pCGN3223 digested with *Xho*I and *Sal*I, resulting in pCGN3229.

pCGN3229 is digested with *Nco*I and *Xho*I to remove the mature desaturase encoding region. The *R. communis* synthase factor A fragment described above is digested with *Nco*I and *Xho*I and ligated to the *Nco*I/*Xho*I digested pCGN3229. This results in pCGN4308, the napin 5'/desaturase:synthase A/napin 3' fusion construct. pCGN4308 is digested with *Asp*718 and subcloned into binary vector pCGN1557 to produce plant transformation construct pCGN4318.

C. Synthase III Constructs

Fusion constructs of the bacterial synthase III encoding sequence and various plant transit peptide encoding sequences may be prepared. These constructs are used for generation of transgenic plants, wherein the bacterial synthase is incorporated into the chloroplasts for interaction with the plant fatty acid synthesis enzymes.

A fusion of the *Brassica* ACP transit peptide encoding sequence from a *B. rapa* (formerly *campestris*) seed ACP cDNA (Rose et al. (1987) *Nuc. Acids Res.* 15:7197) and the β -ketoacyl-acyl carrier protein synthase III gene (*fabH*) from *E. coli* K-12 (Tsay et al. (1992) *J. Biol Chem.* 267:6807-6814), is prepared as follows. The *B. rapa* ACP transit peptide encoding region plus the 5' untranslated sequence is obtained by PCR, wherein the oligonucleotide primers are designed such that an *Bam*HI site is added immediately 5' to the *Xho*I site at the 5' end of the *B. rapa* cDNA clone, and an *Nhe*I site is inserted immediately 3' to the cysteine codon at the 3' end of the transit peptide encoding region. The *fabH* encoding region is obtained by PCR from *E. coli* DNA, with oligonucleotide primers designed such that an *Nhe*I site is inserted immediately 5' to the N-terminal

methionine codon, and *Xho*I and *Sma*I sites are inserted immediately 3' to the TAG stop codon. The *Nhe*I site adds an alanine and serine encoding region immediately 5' to the *fabH* N-terminal methionine.

5 The ACP and synthase III fragments are obtained by ligation at the inserted *Nhe*I restriction sites. The ACP/synthase III fusion fragment is inserted into an appropriate cassette containing plant regulatory regions. For example, for regulation under the napin regulatory
10 regions, the ACP/synthase III fragment is obtained by digestion with *Bgl*II and *Xho*I and ligated into pCGN3223. Similarly, constructs wherein the fusion ACP/synthase III fragment is positioned for control under various other plant regulatory regions may be obtained. Other regulatory
15 regions of interest include the *Bce*4 and ACP regions for seed expression, as well as 35S, double 35S, or T-DNA promoter regions (such as *mas* and *nos*), to provide for constitutive expression in various plant tissues. Constitutive expression may be desirable to test for uptake
20 into chloroplasts of the synthase protein produced by such constructs, for example by electroporation into plant protoplasts and Western analysis. Constitutive expression is also useful for analysis of effects of the expression of synthase in various plant tissues, such as leaves, roots
25 and stems.

Additional ACP/synthase III fusion constructs may be prepared which include various portions of the ACP mature protein encoding region in addition to the ACP transit peptide encoding region. For example, a fusion containing
30 the *B. rapa* ACP transit encoding sequence plus coding sequence for an additional 12 amino acids of the mature ACP protein is prepared. The *fabH* encoding region is obtained by PCR from *E. coli* DNA, with oligonucleotide primers designed such that an *Dde*I site, "CTAAG" is inserted
35 immediately 5' to the N-terminal methionine codon, and *Xho*I and *Sma*I sites are inserted immediately 3' to the TAG stop codon. The *B. rapa* ACP clone contains a *Dde*I site within the codons for amino acids 11-12 (Ser-Lys) of the mature protein region. Thus, the *B. rapa* ACP transit plus 12

fragment is obtained by digestion with *Dde*I and an appropriate site 5' to the ATG start codon. This fragment is ligated to the synthase III fragment at the *Dde*I site to form the ACP transit + 12/synthase III fusion. This fusion is inserted into a napin expression cassette by digestion with *Xho*I and ligation to *Xho*I digested pCGN3223. As discussed above, additional constructs for transcriptional control of the synthase III fusion under various other plant regulatory elements may be similarly prepared.

In addition to the ACP transit peptide discussed above, various other plant transit peptides are known in the art, and may be used in a similar manner. For example, the *Brassica* synthase A transit peptide used above in *R. communis* synthase fusion constructs, may also find use in conjunction with the bacterial synthase III. Similarly, other known transit peptides, such as those for SSU, stearyl ACP desaturase and other nuclear encoded chloroplast proteins may be substituted for the ACP transit peptide.

D. Constructs Containing More than One Synthase Gene

If more than one synthase gene is required to obtain an optimum effect in plants, the genes may be expressed under regulation of the same promoter, or alternatively under regulation of two different promoters that are preferentially expressed in developing seeds, such as the napin, ACP, and Bce4 sequences described above. The constructs may then be introduced into plants in the same binary vector, or introduced simultaneously in different binary vectors.

For example, for expression of both synthase factors A and B in plant cells, a construct is prepared where *R. communis* synthase factor A and *R. communis* synthase factor B genes are each under the control of napin regulatory regions in the same binary vector.

The napin/factor A/napin region of pCGN2785 is obtained by digestion with *Asp*718 and ligated into *Asp*718 digested pCGN1557 (McBride et al.; *supra*), resulting in pCGN2787. pCGN2787 is digested at the unique *Pst*I site and treated with T4 polymerase to fill in the 3' overhang, and

digested with calf intestinal alkaline phosphatase to dephosphorylate the 5' termini to prevent self-ligation of pCGN2787. The napin/factor B/napin region of pCGN2786 is obtained by digestion with HindIII and the Klenow fragment of DNA polymerase to provide a blunt-ended DNA fragment, which is then ligated to the T4 polymerase blunt-ended pCGN2787 DNA. The resulting construct, pCGN2797, contains the *R. communis* synthase factors A and B, each positioned for expression from a napin promoter region.

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Example 5. Plant Transformation

In this example, an *Agrobacterium*-mediated plant transformation is described and *Brassica napus* is exemplified. Also, a DNA-bombardment plant transformation is described and peanut transformation is exemplified.

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A. Agrobacterium Mediated Transformation

Transformation of *Brassica* species is described by Radke et al. (*Theor. Appl. Genet.* (1988) 75:685-694; *Plant Cell Reports* (1992) 11:499-505). Seeds of *Brassica napus* cv. Delta are soaked in 95% ethanol for 2 min, surface sterilized in a 1.0% solution of sodium hypochlorite containing a drop of Tween 20 for 45 min., and rinsed three times in sterile, distilled water. Seeds are then plated in Magenta boxes with 1/10th concentration of Murashige minimal organics medium (Gibco) supplemented with pyridoxine (50 µg/l), nicotinic acid (50 µg/l), glycine (200 µg/l), and 0.6% Phytagar (Gibco) pH 5.8. Seeds are germinated in a culture room at 22°C in a 16 h photoperiod with cool fluorescent and red light of intensity approximately 65 µEinstein per square meter per second (µEm⁻²s⁻¹).

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Hypocotyls are excised from 7 day old seedlings, cut into pieces approximately 4 mm in length, and plated on feeder plates (Horsch et al. 1985). Feeder plates are prepared one day before use by plating 1.0 ml of a tobacco suspension culture onto a petri plate (100x25 mm) containing about 30 ml MS salt base (Carolina Biological) 100 mg/l inositol, 1.3 mg/l thiamine-HCl, 200 mg KH₂PO₄ with 3% sucrose, 2,4-D (1.0 mg/l), 0.6% Phytagar, and pH

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- adjusted to 5.8 prior to autoclaving (MS0/1/0 medium). A sterile filter paper disc (Whatman 3 mm) is placed on top of the feeder layer prior to use. Tobacco suspension cultures are subcultured weekly by transfer of 10 ml of culture into 100 ml fresh MS medium as described for the feeder plates with 2,4-D (0.2 mg/l), Kinetin (0.1 mg/l). All hypocotyl explants are preincubated on feeder plates for 24 h. at 22°C in continuous light of intensity $30 \mu\text{Em}^{-2}\text{s}^{-1}$ to $65 \mu\text{Em}^{-2}\text{s}^{-1}$.
- Single colonies of *A. tumefaciens* strain EHA101 containing a binary plasmid are transferred to 5 ml MG/L broth and grown overnight at 30°C. Per liter, MG/L broth contains 5g mannitol, 1 g L-glutamic acid or 1.15 g sodium glutamate, 0.25 g KH_2PO_4 , 0.10 g NaCl, 0.10 g $\text{MGSO}_4 \cdot 7\text{H}_2\text{O}$, 1 mg biotin, 5 g tryptone, and 2.5 g yeast extract, and the broth is adjusted to pH 7.0. Hypocotyl explants are immersed in 7-12 ml MG/L broth with bacteria diluted to 1×10^8 bacteria/ml and after 10-20 min. are placed onto feeder plates. After 48 h of co-incubation with *Agrobacterium*, the hypocotyl explants are transferred to B5 0/1/0 callus induction medium which contains filter sterilized carbenicillin (500 mg/l, added after autoclaving) and kanamycin sulfate (Boehringer Mannheim) at concentrations of 25 mg/l.
- After 3-7 days in culture at $65 \mu\text{Em}^{-2}\text{s}^{-1}$ to $75 \mu\text{Em}^{-2}\text{s}^{-1}$ continuous light, callus tissue is visible on the cut surface and the hypocotyl explants are transferred to shoot induction medium, B5BZ (B5 salts and vitamins supplemented with 3 mg/l benzylaminopurine, 1 mg/l zeatin, 1% sucrose, 0.6% Phytagar and pH adjusted to 5.8). This medium also contains carbenicillin (500 mg/l) and kanamycin sulfate (25 mg/l). Hypocotyl explants are subcultured onto fresh shoot induction medium every two weeks.

- Shoots regenerate from the hypocotyl calli after one to three months. Green shoots at least 1 cm tall are excised from the calli and placed on medium containing B5 salts and vitamins, 1% sucrose, carbenicillin (300 mg/l), kanamycin sulfate (50 mg/l) and 0.6% Phytagar) and placed in a culture room with conditions as described for seed

germination. After 2-4 weeks shoots which remain green are cut at the base and transferred to Magenta boxes containing root induction medium (B5 salts and vitamins, 1% sucrose, 2 mg/l indolebutyric acid, 50 mg/l kanamycin sulfate and 0.6% 5 Phytagar). Green rooted shoots are tested for NPT II activity.

Transgenic *Arabidopsis thaliana* plants may also be obtained by *Agrobacterium*-mediated transformation using similar techniques. For example, a useful method has been 10 described by Valverkens et al., (*Proc. Nat. Acad. Sci.* (1988) 85:5536-5540).

B. Transformation by Particle Bombardment

DNA sequences of interest may be introduced as expression cassettes, comprising at least a promoter 15 region, a gene of interest, and a termination region, into a plant genome via particle bombardment as described in European Patent Application 332 855 and in co-pending application USSN 07/225,332, filed July 27, 1988.

Briefly, tungsten or gold particles of a size ranging 20 from 0.5 μ M-3 μ M are coated with DNA of an expression cassette. This DNA may be in the form of an aqueous mixture or a dry DNA/particle precipitate.

Tissue used as the target for bombardment may be from cotyledonary explants, shoot meristems, immature leaflets, 25 or anthers.

The bombardment of the tissue with the DNA-coated particles is carried out using a Biolistics™ particle gun (Dupont; Wilmington, DE). The particles are placed in the barrel at variable distances ranging from 1cm-14cm from the 30 barrel mouth. The tissue to be bombarded is placed beneath the stopping plate; testing is performed on the tissue at distances up to 20 cm. At the moment of discharge, the tissue is protected by a nylon net or a combination of nylon nets with mesh ranging from 10 μ M to 300 μ M.

35 Following bombardment, plants may be regenerated following the method of Atreya, et al., (*Plant Science Letters* (1984) 34:379-383). Briefly, embryo axis tissue or cotyledon segments are placed on MS medium (Murashige and Skoog, *Physio. Plant.* (1962) 15:473) (MS plus 2.0 mg.l 6-

benzyladenine (BA) for the cotyledon segments) and incubated in the dark for 1 week at $25 \pm 2^\circ\text{C}$ and are subsequently transferred to continuous cool white fluorescent light (6.8 W/m^2). On the 10th day of culture, the plantlets are transferred to pots containing sterile soil, are kept in the shade for 3-5 days and finally moved to greenhouse.

The putative transgenic shoots are rooted. Integration of exogenous DNA into the plant genome may be confirmed by various methods known to those skilled in the art.

Example 6. Analysis of Transformed Plants

Seeds from 15 *Arabidopsis* plants transformed with pCGN2797 (napin 5'/*R. communis* synthase factor A/napin 3' and napin 5'/*R. communis* synthase factor B/napin 3') were analyzed for the presence of *R. communis* synthase proteins. Five of these plants test positive, by Western analysis, for expression of the 50kD *R. communis* synthase factor B protein. Cross-reactivity of the *R. communis* synthase factor A polyclonal antibody with the corresponding *Brassica* synthase protein, prevents detection of this synthase protein by Western analysis.

Two of the plants which tested positive for expression of the 50kD *R. communis* synthase protein, transformants #5 and #6 have been analysed to determine the fatty acid composition of their seed oil. Several non-expressing transformants and a non-transformed control were similarly analyzed. Seed fatty acid composition is determined by the acid methanolysis method according essentially as described by Browse et al. (*Anal. Biochem.* (1986) 152:141-145). Briefly, 100 seeds of each sample are treated with 1 ml of 5% H_2SO_4 in MeOH and heated in a 90°C water bath for two hours to convert the fatty acids to fatty acid methyl esters (FAMES). An internal standard (C17:0) is added to each sample (250ml of a 1mg/ml solution in toluene) prior to the heating step. The samples are allowed to cool, after which 1 ml 0.9% NaCl in H_2O is added to aid in phase separation. Hexane (250ml to each vial) is added to

extract the FAMES, and the samples are then vortexed and centrifuged to separate the phases. The hexane layer is removed and transferred to a GC autosampler for injected on the GC. A useful GC temperature program for these analyses is as follows: 200°C for zero minutes, followed by a 5 degrees per minute temperature ramp to a final temperature of 250°C, which is held for 6 minutes. Data is reported as % of total fatty acids in Table I below.

Seeds from transformant #5 contain 3.95% C16:0, and seeds from #6 have a 4.59% C16:0. Seeds from the non-expressing transformants and the non-transformed control had C16:0 percentages ranging from 5.85 to 6.63%. Total saturated fatty acids in seeds from #5 were 9.74%, compared to 12.47% total saturated fatty acids for seeds from the non-transformed control and a range of 11.57%-13.33% total saturated fatty acids for seeds from the non-expressing transformants. The total saturated fatty acid level in transformant #6 is 10.64%.

TABLE I

SAMPLE:	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0	22:1	22:2	24:0	SATS
	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%
1	0.03	0.08	6.22	0.24	3.11	18.10	25.36	18.56	2.44	21.16	1.81	0.34	2.21	0.10	0.23	12.44
3	0.08	0.09	6.08	0.24	3.02	18.62	25.21	18.75	2.26	21.21	1.70	0.31	2.09	0.12	0.21	12.06
5	0.09	0.07	3.95	0.20	2.77	17.68	27.99	18.82	2.30	20.58	2.13	0.35	2.69	0.16	0.21	9.74
6	0.01	0.07	4.59	0.18	3.15	20.95	25.30	17.71	2.28	21.33	1.75	0.32	2.04	0.09	0.22	10.64
9	0.01	0.08	5.85	0.25	2.89	19.24	25.98	17.46	2.23	21.43	1.80	0.33	2.14	0.14	0.19	11.57
10	0.11	0.12	6.63	0.33	3.14	16.48	27.66	17.07	2.71	20.59	2.16	0.38	2.24	0.14	0.24	13.33
11	0.07	0.08	6.01	0.24	3.04	19.43	24.93	17.86	2.36	21.47	1.81	0.32	2.07	0.09	0.21	12.10
12	0.01	0.08	5.91	0.21	3.09	19.98	24.28	18.84	2.23	21.16	1.59	0.33	2.02	0.09	0.18	11.83
15	0.01	0.07	5.88	0.20	3.22	20.85	24.05	18.72	2.30	20.83	1.59	0.30	1.75	0.06	0.16	11.94
CONTROL:	0.01	0.09	6.33	0.28	3.12	18.15	25.77	19.37	2.35	19.85	2.00	0.35	2.00	0.11	0.21	12.47

The above results demonstrate the ability to use synthase DNA sequences in plant genetic engineering methods for production of transgenic plants having modified seed oil compositions.

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All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein

10 incorporated by referenced to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

15 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claim.

What is claimed is:

1. A recombinant DNA construct comprising, in the 5' to 3' direction of transcription, a promoter functional in a plant cell, a β -ketoacyl-ACP synthase protein encoding sequence and a transcriptional termination regulatory region 3' to said synthase protein encoding sequence, wherein said β -ketoacyl-ACP synthase protein is from a non-plant source.
2. The construct of Claim 1, wherein said synthase protein encoding sequence is oriented for transcription of a sense sequence.
3. The construct of Claim 2, wherein said construct comprises, immediately 5' to said synthase protein encoding sequence, a plant sequence encoding a transit peptide.
4. The construct of Claim 3, wherein said synthase protein encoding sequence is the *E. coli fabH* gene sequence.
5. The construct of Claim 3, wherein said transit peptide encoding sequence is from an acyl-carrier protein gene.
6. The construct of Claim 1 wherein said promoter is from a gene that is preferentially expressed in plant seed tissue.
7. A plant cell comprising a construct according to Claim 1.
8. The plant cell of Claim 7 further comprising a second recombinant DNA construct providing for transcription in said plant cell of a substantial portion of a sequence encoding a protein associated with lipid synthesis.
9. The cell of Claim 8 wherein said protein is a desaturase or a thioesterase.
10. The cell of Claim 7 or 8 wherein said plant cell is a *Brassica* plant cell.
11. A recombinant DNA construct comprising, in the 5' to 3' direction of transcription, a promoter functional in a plant cell, a plant transit peptide encoding sequence, a mature *R. communis* β -ketoacyl-ACP synthase factor A encoding sequence and a transcriptional termination

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regulatory region 3' to said synthase protein encoding sequence, wherein said transit peptide encoding sequence is not naturally associated with said *R. communis* β -ketoacyl-ACP synthase factor A encoding sequence.

5 12. The construct of Claim 11, wherein said plant transit peptide encoding sequence is from a gene encoding a *Brassica* β -ketoacyl-ACP synthase protein.

13. The construct of Claim 12, wherein said *Brassica* synthase protein is synthase factor A.

10 14. The construct of Claim 11, wherein said plant transit peptide encoding sequence is from a gene encoding a stearoyl-ACP desaturase protein.

15 15. A plant cell comprising a construct according to Claim 11.

16. The cell of Claim 15 wherein said plant cell is a *Brassica* plant cell.

17. A transgenic plant cell comprising a non-plant β -ketoacyl-ACP synthase protein expressed from a recombinant DNA sequence.

20 18. The cell of Claim 17 wherein said non-plant synthase protein is the β -ketoacyl-ACP synthase protein encoded by *E. coli fabH*.

25 19. A method of producing a non-plant β -ketoacyl-ACP synthase protein in a plant cell or progeny thereof comprising

growing a plant cell or progeny thereof comprising a construct according to Claim 1, under conditions which will permit the production of said β -ketoacyl-ACP synthase protein.

30 20. A plant cell comprising a non-plant β -ketoacyl-ACP synthase protein produced according to Claim 19.

21. A plant cell of Claim 20 wherein said construct is integrated into the genome of said plant cell.

35 22. A method of modifying the fatty acid composition in a plant cell comprising:

growing a plant cell having integrated in its genome a DNA construct, said construct comprising in the 5' to 3' direction of transcription, a promoter functional in said plant cell, a non-plant β -ketoacyl-ACP synthase

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protein encoding sequence, and a transcriptional termination region functional in said plant cell, under conditions which will permit the expression of said synthase protein encoding sequence.

5 23. The method of Claim 22 wherein said synthase protein encoding sequence is a sense sequence.

24. The method of Claim 23 wherein said synthase protein is the β -ketoacyl-ACP synthase protein encoded by *E. coli fabH*.

10 25. A method of modifying the fatty acid composition in a plant cell comprising:

growing a plant cell having integrated in its genome a DNA construct according to Claim 11, under conditions which will permit the transcription of said synthase protein encoding sequence.

15 26. The method of Claim 22 or 25 wherein said plant cell is an oilseed plant seed cell.

27. A plant cell having a modified free fatty acid composition produced according to the method of Claim 26.

20 28. A plant seed having a modified fatty acid composition as compared to a seed of said plant having a native fatty acid composition, produced according to a method comprising:

growing a plant to seed, wherein said plant has integrated in its genome a recombinant DNA sequence comprising a non-plant β -ketoacyl-ACP synthase protein encoding sequence under the transcriptional control of regulatory elements functional in seed during lipid accumulation, under conditions which will promote the activity of said regulatory elements, and

30 harvesting said seed.

29. The seed of Claim 28 wherein said synthase protein is the β -ketoacyl-ACP synthase protein encoded by *E. coli fabH*.

35 30. A plant seed having a modified fatty acid composition as compared to a seed of said plant having a native fatty acid composition, produced according to a method comprising:

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growing a plant to seed, wherein said plant has integrated in its genome a recombinant DNA construct according to Claim 11, under conditions which will promote the activity of said regulatory elements, and

5 harvesting said seed.

31. The seed of Claim 28 or 30 wherein said plant is an oilseed plant.

32. The seed of Claim 31 wherein said plant is *Brassica*.

10 33. A method of modifying the fatty acid composition of triglycerides produced from an oilseed crop plant comprising:

growing a plant cell having integrated in its genome a DNA construct, said construct comprising in the 5' to 3' direction of transcription, a promoter functional in
15 said plant cell and a non-plant β -ketoacyl-ACP synthase protein encoding sequence, under conditions which will permit the transcription of said synthase protein encoding sequence.

20 34. The method of Claim 33 wherein said synthase protein encoding sequence is a sense sequence.

35. The method of Claim 34 wherein said synthase protein is the β -ketoacyl-ACP synthase protein encoded by *E. coli fabH*.

25 36. A method of modifying the fatty acid composition of triglycerides produced from an oilseed crop plant comprising:

growing a plant cell having integrated in its genome a DNA construct according to Claim 11, under
30 conditions which will permit the transcription of said synthase protein encoding sequence.

37. The method of Claim 33 or 36 wherein said plant cell is a seed cell.

38. A plant cell having a modified fatty acid
35 composition of triglycerides produced according to the method of Claim 37.

39. The method of Claim 37 wherein said oilseed crop plant is selected from the group consisting of rapeseed,

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sunflower, safflower, cotton, cuphea, soybean, peanut,
coconut, oil palm and corn.

40. A plant seed oil separated from a seed produced
according to Claim 31.

5 41. The oil of Claim 40, wherein said plant is
Brassica.

1137

1 GGCTTCTCCCAATTCATCGTTTGGATCGCTACCACTTCGGCCACCACCCACCACCATGCAAGCCCTGC 69
 METGlnAlaLeuG

 PstI
 70 AGTCCCGTCTCTCCGACCATCCCCTCTAACCCCGCTCCATAAAAATACTCACAATGCAGCAAAACGCC 138
 InSerProSerLeuArgProSerProLeuThrProLeuHisLysAsnThrHisAsnAlaAlaLysArgP

 139 CAACTAAAAGGTCTCCTTTATCACCGCATCATCAACAAATAACAACACGACGATTTTCAGCTCCAAAGC 207
 roThrLysLysValSerPheIleThrAlaSerSerThrAsnAsnThrThrIleSerAlaProLysA

 208 GAGAGAAAGACCCAGAAAAGGGTAGTCATAACTGTACGGGTTTGGTATCTGTGTTTGGGAATGATG 276
 rgGluLysAspProArgLysArgValIleThrGlyThrGlyLeuValSerValPheGlyAsnAspV

 277 TCGATACTTACTACGATAAATTGCTTGCTGGAGAAAGTGGATCGGACTTATTGATAGGTTTCGATGCGT 345
 alAspThrTyrTyrAspLysLeuLeuAlaGlyGluSerGlyIleGlyLeuIleaspArgPheAspAlas

 346 CTAAGTTTCCTACTAGATTTGGTGGACAGATCAGGGGGTTTAATTCACCTTGGTTATATTGATGGGAAA 414
 erLysPheProThrArgPheGlyGlyGlnIleArgGlyPheAsnSerLeuGlyTyrIleAspGlyLysA

FIG. 1A

SphI
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415 ATGATAGAAGGCTTGATGATTGTTGAGGTATTGCATTGTTGCTGGTAAAAAGCTCTTGAGCATGCTG 483
snAspArgArgLeuAspCysLeuArgTyrCysIleValAlaGlyLysLysAlaLeuGluHisAlaa

484 ATCTTGGTGGTGATAAGTTGCTAAGATTGATAAAGAGCGAGCTGGTGTGCTTGTGGAAACAGGGATGG 552
spLeuGlyGlyAspLysLeuSerLysIleAspLysGluArgAlaGlyValLeuValGlyThrGlyMETG

553 GTGGTCTTACAGTCTTTTCAGATGGTGTTCAGGCCCTAATTGAAAAAGGACACAGGAAAAATTACCCCAT 621
lyGlyLeuThrValPheSerAspGlyValGlnAlaLeuIleGluLysGlyHisArgLysIleThrProp

622 TCTTTATTCTTATGCTATAACAAACATGGGATCTGCCCTTGTAGCTATTGAACCTTGGTCTCATGGGTC 690
hePheIleProTyrAlaIleThrAsnMETGlySerAlaLeuAlaIleGluLeuGlyLeuMETGlyP

691 CTAATTATTCAATTCAACTGCTTGTGCTACCTCCAATTATTGCTTCTATGCTGCTGCCAATCATATTC 759
roAsnTyrSerIleSerThrAlaCysAlaThrSerAsnTyrCysPheTyrAlaAlaAsnHisIleA

760 GCAGAGGTGAGGCTGAATTGATGATTGCTGGTGGAACTGAAGCCGCCCATCATTCCAATCGGTTGGGAG 828
rgArgGlyGluAlaGluLeuMETIleAlaGlyGlyThrGluAlaAlaIleIleProIleGlyLeuGlyG

FIG. 1B

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NcoI
 829 GTTTTGTAGCATGTAGGGCCTTATCACAAGGAATGATGATCCACAACTGCCTCAAGGCCATGGGACA 897
 lyPheValAlaCysArgAlaLeuSerGlnArgAsnAspProGlnThrAlaSerArgProTrpAspL
 898 AAGATCGAGATGGCTTTGTTATGGGTGAAGGTGCTGGAGTGTGGTAATGGAGAGTTTGGAAACATGCAA 966
 ysAspArgAspGlyPheValMETGlyGluGlyAlaGlyValLeuValMETGluSerLeuGluHisAlaM
 ScaI
 967 TGAAGAGGGGTGCACCAATAATTGCTGAGTACTTGGGAGGTGCTGTTAATTGTGATGCTTATCACATGA 1035
 ETLysArgGlyAlaProIleIleAlaGluTyrLeuGlyGlyAlaValAsnCysAspAlaTyrHisMETT
 997
 1036 CTGATCCAAGGGCTGATGGACTTGGGGTCTCTTCCTGCATTGAGAGAAAGTCTTGAAGATGCCGGTGTGT 1104
 hrAspProArgAlaAspGlyLeuGlyValSerSerCysIleGluArgSerLeuGluAspAlaGlyValS
 HpaI
 1105 CACCTGAGGAGGTTAACTATATAATGCACATGCACAACTTCCACTCTTGTGCTGTGACCTTCTGAGATAA 1173
 erProGluGluValAsnTyrIleAsnAlaHisAlaThrSerThrLeuAlaGlyAspLeu GluIleA
 1119

FIG. 1C

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1174 ATGCTATTAAAAAGTATTCAAGAAATACGTCTGACATCAAAATCAATGCAACCAAGTCTATGATAGGAC 1242
snAlaIleLysLysValPheLysAsnThrSerAspIleLysIleAsnAlaThrLysSerMETIleGlyH

1243 ATTGCCTTGGTGCTGCTGGAGGCTCTGGAAGCAATTGCCTGTGTGAAGGCCATTACCACAGGATGGTTGC 1311
isCysLeuGlyAlaAlaGlyGlyLeuGluAlaIleAlaCysValLysAlaIleThrThrGlyTrpLeuH

1312 ATCCTACAATTAAATCAATTTAACCAGAGCCATCAGTTGAATTTGACACTGTGCTGCAATAAAGAAGCAGC 1380
isProThrIleAsnGlnPheAsnProGluProSerValGluPheAspThrValAlaAsnLysLysGlnG

1381 AGCACGAAGTGAATGTTGCCATTTCAAATTCCTTTGGATTCCGGTGGACACAACTCTGTGGTAGCCTTTT 1449
lnHisGluValAsnValAlaIleSerAsnSerPheGlyPheGlyGlyHisAsnSerValValAlaPheS

1450 CTGCATTTAAACCCTGAGAGCATGGTTTTTCTTCTGCATTCCGGCCCGGGTCATTATACCATGGC 1518
exAlaPheLysPro .
NcoI
| - |

1519 CTGCATTTCTGTAGGAACCACTGGAGAGTTGCTTGCTTATAGACAGAGTCATCGACATCACTTCCCCC 1587

1588 TTTTAGCTTTTGTAGCTGCTGATAGTAGTCAGTTTCTCATTTTCAGTATCAAGTCTATCTTAAGAAGGTC 1656

1657 TTGCTTATTTTCTTT 1672

FIG. 1D

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1 GGCTTCTCCCAATTCATCGTTGTTATCGCTACCACTTCCGCCACCAACCCACCACTGCAAGCCCTGC 69
 LeuLeuProIleHisArgCysTyrArgTyrHisPheArgHisHisProThrThrMETGlnAlaLeuG

70 AGTCCCCGTCTCTCCGACCATCCCTCTAACCCTCCGCTCCATAAAAATACTCACAATGCAGCAAAACGCC 138
 InSerProSerLeuArgProSerProLeuThrProLeuHisLysAsnThrHisAsnAlaAlaLysArgP

139 CAACTAAAAAGGTCCTCTTTATCACCGCATCATCAACAATAACAACACGACGATTTTCAGCTCCAAAGC 207
 roThrLysLysValSerPheIleThrAlaSerSerThrAsnAsnAsnThrThrIleSerAlaProLysA

208 GAGAGAAAGACCCAGAAAAAGGGTAGTCATAACTGGTACGGGTTTGGTATCTGTGTGTTGGGAATGATG 276
 rgGluLysAspProArgLysArgValValIleThrGlyThrGlyLeuValSerValPheGlyAsnAspV

277 TCGATACTTACTACGATAAATTGCTTGCTGGAGAAAGTGGATCGGACTTATTGATAGTTCCGATGCGT 345
 alAspThrTyrTyrAspLysLeuAlaGlyGluSerGlyIleGlyLeuIleAspArgPheAspAlas

346 CTAAAGTTTCTACTAGATTTGGTGGACAGATCAGGGGGTTTAATTCACAAGGTTATATTGATGGGAAA 414
 erLysPheProThrArgPheGlyGlyGlnIleArgGlyPheAsnSerGlnGlyTyrIleAspGlyLysA

415 ATGATAGAAGGCTTGATGATTGTTGAGGTATTGTCATTGTTGCTGTGTAATAAGCTCTTGAGCATGCTG 483
 snAspArgArgLeuAspAspCysLeuArgTyrCysIleValAlaGlyLysLysAlaLeuGluHisAlaa

FIG. 2A

6137

484 ATCTTGGTGTGATAAGTTGTCTAAGATTGATAAAGACGAGCTGTGTGCTTGTGGAACAGGGATGG 552
spLeuGlyGlyAspLysLeuSerLysIleAspLysGluArgAlaGlyValLeuValGlyThrGlyMETG

553 GTGGTCTTACAGTCTTTTCAGATGGTGTTCAGGCCCTAATTGAAAAAGACACAGGAAAATTACCCCAT 621
lyGlyLeuThrValPheSerAspGlyValGlnAlaLeuIleGluLysGlyHisArgLysIleThrProp

622 TCTTTATTCCTTATGCTATAACAAACATGGGATCTGCCCTTGTAGCTATTGAACCTTGGTCTCATGGGTC 690
hePheIleProTyrAlaIleThrAsnMETGlySerAlaLeuAlaIleGluLeuGlyLeuMETGlyLP

691 CTAATTATTCAATTCAACTGCTTGTGCTACCTCCAATTATTGCTTCTATGCTGCTGCCAATCATATTC 759
roAsnTyrSerIleSerThrAlaCysAlaThrSerAsnTyrCysPheTyrAlaAlaAlaAsnHisIleA

760 GCAGAGGTGAGGCTGAATTGATGATTGCTGGTGAACCTGAAGCCGCCCATCATTCCAATCGGTTTGGGAG 828
rgArgGlyGluAlaGluLeuMETIleAlaGlyGlyThrGluAlaAlaIleIleProIleGlyLeuGlyG

829 GTTTTGTAGCATGTAGGCCCTTATCACAAAGGAATGATGATCCACAAACTGCCCTCAAGGCCATGGGACA 897
lyPheValAlaCysArgAlaLeuSerGlnArgAsnAspProGlnThrAlaSerArgProTrpAspL

898 AAGATCGAGATGGCTTTTGTATGGGTGAAGGTGCTGGAGTGTGGTAATGGAGAGTTTGGAAACATGCAA 966
ysAspArgAspGlyPheValMETGlyGluGlyAlaGlyValLeuValMETGluSerLeuGluHisAlaM

FIG. 2B

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967 TGAAAAGGGGTGCACCAATAATTGCTGAGTACTTGGGAGGTGCTGTTAATTGTGATGCTTATCACAATGA 1035
ETLysArgGlyAlaProIleAlaGluTyrLeuGlyGlyAlaValAsnCysAspAlaTyrHisMETT

1036 CTGATCCAAGGGCTGATGGACTTGGGGTCTCTTCCTGCATTGAGAGAAGTCTTGAAGATGCCCGGTGTGT 1104
hrAspProArgAlaAspGlyLeuGlyValSerSerCysIleGluArgSerLeuGluAspAlaGlyValS

1105 CACCTGAGGAGGTTAACTATATAAATGCACATGCAACTTCCACTCTTGTGCTGGTGACCTTGTGAGATAA 1173
erProGluGluValAsnTyrIleAsnAlaHisAlaThrSerThrLeuAlaGlyAspLeuAlaGluIleA

1174 ATGCTATTAAAAAGTATTCAAGAATACGTCTGACATCAAAATCAATGCAACCAAGTCTATGATAGAC 1242
snAlaIleLysLysValPheLysAsnThrSerAspIleLysIleAsnAlaThrLysSerMETIleGlyH

1243 ATTGCCCTTGGTGCTGGAGGTCTGGAAGCAATTGCCCTGTGTGAAGGCCATTACCACAGGATGGTTGC 1311
isCysLeuGlyAlaAlaGlyGlyLeuGluAlaIleAlaCysValLysAlaIleThrThrGlyTrpLeuH

1312 ATCTACAATTAATCAATTAAACCAGAGCCATCAGTTGAATTTGACACTGTTGCCAATAAGAAGCAGC 1380
isProThrIleAsnGlnPheAsnProGluProSerValGluPheAspThrValAlaAsnLysLysGlnG

1381 AGCACGAAGTGAATGTTGCCATTTCAAATTCTTTGGATTTCGGTGGACACAACCTCTGTGGTAGCCTTTT 1449
lnHisGluValAsnValAlaIleSerAsnSerPheGlyPheGlyGlyHisAsnSerValValAlaPheS

FIG. 2C

1450 CTGCATTTAAACCCTGAGAGCATGGCCCTTCTTCTGCATTGCGGGCCGCGGTCAATTTACATTTACCATGGC 1518
erAlaPheLysPro

1519 CTGCATTCTTGTAGGAACCACTGGAGAGTTGCTTATAGACAGAGTCATCGACATCACTTCCCCC 1587

1588 TTTTAGCTTTTGTAGCTGCTGATAGTAGTCAGTTTCTCATTTTCAGTATCAAGTCTATCTTAAGAAAGTC 1656

1657 TTGCTTAATTTTCTTTTCAAAATTACCATTTTCATTTGTCATTTTCTTGGAACTTTTAGCTTAAGATCTG 1725

1726 CTGTGATCATGTGGTTTGTGATTTCAAAATTAATTATGTAGCGGATACGAAACAAGCAATCATAAAAAAGTCT 1794

1795 TTTTGAATTATGTAATTACGATAAAGTATTCTTTTCTTTTCAAAAAAAA 1845

8137

FIG. 2D

9137

1 CCCCGTGGCGGCGTGCATGTGCGTCACGTGCTCAAAGGAGAACAGACACGCGTTCTTCTTCATCGAC 69
ProValAlaAlaCysMETSerValThrCysSerLysGluAsnArgHisAlaPhePheSerSerTh

70 ACCGGGCACACAGCAGTCACAGTCGTACAGAGGAGGCGCTAAATATAATAGTATCAGCACCCCTGC 138
rProGlyThrThrSerSerHisSerArgThrArgArgProLysTyrAsnSerIleSerThrProAl

139 CTCTCAATCTTCTTTAATTCTTATCATCTTCTGGATCGAGTTTCAACAATAATGTCTTCTTGCTT 207
aSerGlnSerPhePheAsnSerLeuSerSerSerGlySerSerPheGlnGlnLeuMETSerSerCysLe

208 GGCCTTCGAGCCTTGTAGTCATTACTACAGCTCTAATGGCCTCTTTCCTAACACTCCTCTTCTCTAA 276
uAlaPheGluProCysSerHisTyrTyrSerSerAsnGlyLeuPheProAsnThrProLeuLeuProLy

277 GCGCCATCCTAGACTTCATCATCGCCTTCCCTGTTCTGGGAAGCAATGGCAGTGGCTGTCAACCTGA 345
sArgHisProArgLeuHisHisArgLeuProArgSerGlyGluAlaMETAlaValAlaValGlnProGl

346 AAAGGAGGTTGCAACAATAAGAAACCTCTTATGAAGCAAAGGAGAGTAGTTGTTACTGGGATGGGTGT 414
uLysGluValAlaThrAsnLysLysProLeuMETLysGlnArgArgValValThrGlyMETGlyVa

415 TGTTTACCCCTTGGTCATGATATAGACGTCTATTACAATAATCTTGTACGGTTCTAGTGGTATTAG 483
lValSerProLeuGlyHisAspIleAspValTyrTyrAsnAsnLeuLeuAspGlySerSerGlyIleSe

FIG. 3A

10137

484 TCAGATTGATTCCTTTGACTGTGCCCAATTTCCCTACGAGGATTGCTGGAGAGATCAAGTCTTTCTCAAC 552
rGlnIleAspSerPheAspCysAlaGlnPheProThrArgIleAlaGlyGluIleLysSerPheSerTh

553 TGATGGATGGTTGCACCAAACTTTCCAAGAGAATGGATAAATTCATGCTTTACATGCTTACTGCTGG 621
rAspGlyTrpValAlaProLysLeuSerLysArgMETAspLysPheMETLeuTyrMETLeuThrAlaGl

622 CAAAAAGCCTTGGCAGATGGTGGTATTACAGAGGATATGATGGATGAATTGGATAAAGCTAGATGTGG 690
yLysLysAlaLeuAlaAspGlyGlyIleThrGluAspMETAspGluLeuAspLysAlaargCysGl

691 AGTTTAAATTGTTCTGCAATGGGTGGCATGAAGTTTTCATGATGCAATTGAAGCATTAAGGATCTC 759
yValLeuIleGlySerAlaMETGlyGlyMETLysValPheAsnAspAlaIleGluAlaLeuargIleSe

760 GTATAGGAAGATGAATCCTTTCTGCGTACCTTTTGGGACTACAAATATGGGCTCTGCCATGCTTGCAAT 828
rTyrArgLysMETAsnPropheCysValPropheAlaThrThrAsnMETGlySerAlaMETLeuAlaME

829 GGACCTTGGTTGGATGGGGCCAACTATTCAATATCTACTGCTTGTGCTACTAGCAATTTTGTATATT 897
TAspLeuGlyTrpMETGlyProAsnTyrSerIleSerThrAlaCysAlaThrSerAsnPheCysIleLe

898 GAATGCCGCAAAACACATCATTAGAGCGAAGCTGATATTATGCTTTGTGGTCTCAGATGCAGCAAT 966
uAsnAlaAlaAsnHisIleIleArgGlyGluAlaAspIleMETLeuCysGlyGlySerAspAlaAlaI

FIG. 3B

967 TATACCTATTGGCTTGGAGGTTTGTGGCATGCAGACGGCTCTCACAGAGGAATGATGATCCTACAAA 1035
eileProilleGlyLeuGlyGlyPheValAlaCysArgAlaLeuSerGlnArgAsnAspProThrLy

1036 AGCTTCACGACCTTGGGATATGAATCGGGATGGATTGTGATGGGGAGGAGCTGGTGTCTTCTTTT 1104
sAlaSerArgProTrpAspMETAsnArgAspGlyPheValMETGlyGluGlyAlaGlyValLeuLeuLe

1105 AGAAGAACTAGAACATGCTAAGAAAAGAGGTGCAATATTTATGCGGAATTTCTTGGAGGAAGCTTTTAC 1173
uGluGluLeuGluHisAlaLysLysArgGlyAlaAsnilleTyrAlaGluPheLeuGlyGlySerPheTh

1174 ATGTGATGCTTATCACATGACTGAACCGCGTCCAGATGGAGTTGGTGTCTCTCTGTATAGAAAAGGC 1242
rCysAspAlaTyrHisMETThrGluProArgProAspGlyValGlyValilleLeuCysilleGluLysAl

1243 ATTAGCGCGATCTGGTGTATCCAAGGAGGAAGTAACTACATAAATGCACATGCTACGTCTACCCAGC 1311
aLeuAlaArgSerGlyValSerLysGluGluValAsnTyrilleAsnAlaHisAlaThrSerThrProAl

1312 TGGAGACCTTAAAGAATATGAAGCTCTTATGCGCTGTTTCAGCCAAAATCCTGATTGAGAGTGAATC 1380
aGlyAspLeuLysGluTyrGluAlaLeuMETArgCysPheSerGlnAsnProAspLeuArgValAsnSe

1381 TACGAAGTCTATGATTGGCCATTACTAGGAGCAGCTGGTGTGGAGCTATAGCAACAATACAGGC 1449
rThrLysSerMETilleGlyHisLeuLeuGlyAlaAlaGlyAlaValGluAlaIleAlaThrilleGlnAl

11137

FIG. 3C

12|37

1450 GATACGGACAGGATGGGTTTCATCCAAACATCAACCTGGAACCCAGAAAGCGGTGGACACAAAGGT 1518
aIleArgThrGlyTrrpValHisProAsnIleAsnLeuGluAsnProGluGluGlyValAspThrLysVa
1519 GCTGGTTGGCCCCAAAGAAGGAGAGATTGGACATTAAAGTTGCTCTGTCCAACTCTTTTGGGTTCCGGTGG 1587
lLeuValGlyProLysLysGluArgLeuAspIleLysValAlaLeuSerAsnSerPheGlyPheGlyG1
1588 GCACAACTCATCGATCATTTTGTGCTCCGTACAAGTGAAATAAGGGGTACTTCAACTTTGGTGTATTAAAC 1656
yHisAsnSerSerIleIlePheAlaProTyrLys
1657 GTGAAAGATGATCTAAAATGGAACAAGATTAGATAACTCTATGGGTAGGAAAGAGAAATATGCCGAGT 1725
1726 TCACAGAGAGGAAACTTCCCGTGAAGATTCCCTGTGCCTTCTACCATTTTCAGTATTCTCTCCGCATCAT 1794
1795 TGTGGCTTGATCCCATGTTGATCCCATCCGAATACCAGTAACAGTGGCCTTATTTAAATTTTGTTCATGTA 1863
1864 TAAGCAGACGGCTGATCGTTGCTTTTAACAGTCAATTGTAATGAATTTTGTAGCTGGACAGTTGGCTAGG 1932
1933 TTACACTAATGTAATGGTGGTTTATGAGCAAAAAA 1969

FIG. 3D

1 ATCGAGACAGCCACGAGAAGCGCTCATTCACTCCGCGTCCTCCGCGTCTCCGCCCCCAAC 69
 AlaArgGlnProThrArgArgSerPheIleSerAlaSerSerAlaValSerAlaProLysA
 70 GCGAAACAGACCCGAAACGGGTCGTAATCACCGGAATGGGCCCTCGTCTCCGTCTTCGGAAACGACG 138
 rgGluThrAspProLysLysArgValValIleThrGlyMETGlyLeuValSerValPheGlyAsnAspV
 139 TCGACGCTTACTACGAGAAGCTGCTCTCCGGCGAGAGTGGAATCAGCTTGATTGATCGGTTTCGACGCCT 207
 alAspAlaTyrTyrGluLysLeuLeuSerGlyGluSerGlyIleSerLeuIleAspArgPheAspAlaS
 208 CCAAGTCCCGACCCGATTCCGGTGACAGATCCCGTGGGTTTCAGCTCAGAGGGTTACATCGATGGGAAGA 276
 erLysPheProThrArgPheGlyGlyGlnIleArgGlyPheSerSerGluGlyTyrIleAspGlyLysA
 277 ATGAGCGGAGGCTTGATGATTGCTTGAAGTACTGCATTGTCGCTGGGAAGAAGGCTCTTGAAAGTGCGA 345
 snGluArgArgLeuAspAspCysLeuLysTyrCysIleValAlaGlyLysLysAlaLeuGluSerAlaA
 346 ATCTTGGTGGTGATAAGCTTAACACGATTGATAAGCAGAAAGCTGGAGTACTAGTTGGGACTGGTATGG 414
 snLeuGlyGlyAspLysLeuAsnThrIleAspLysGlnLysAlaGlyValLeuValGlyThrGlyMETG
 415 GTGGCTTGACTGTGTTTTTCAGACGGGTGTTCAAGCTCTTATTGAGAAAGGTCACAGGAGGATTTCTCCTT 483
 lyGlyLeuThrValPheSerAspGlyValGlnAlaLeuIleGluLysGlyHisArgArgIleSerProp

13137

FIG. 4A

14/37

552
484 TCCTTATTCCTTATGCTATTACAAACATGGGTTCTGCTTGTGGCGATTGATCTTGGTCTTATGGGTC
hepheilleProTyrAlaIleThrAsnMETGlySerAlaLeuAlaIleAspLeuGlyLeuMETGlyP
621
553 CTAACACTACGATCTCGACGGCTTGTGCCACTTCTAACTACTGCTTTTACGCTGCTGCCAATCACATTC
roAsnTyrSerIleSerThrAlaCysAlaThrSerAsnTyrCysPheTyrAlaAlaAlaAsnHisIleA
690
622 GACGTGGTGAAGCTGATATGATAGCTGGTGAACCGAGGCTGCTATTATTCCTATTGGTTTGGGAG
rArgGlyGluAlaAspMETMETIleAlaGlyGlyThrGluAlaAlaIleIleProIleGlyLeuGlyG
759
691 GTTTTGTGCTTGTAGGGCGCTTTCACAGAGAAATGATGATCCTCAGACGGCTTCAAGGCCGTGGGATA
lyPheValAlaCysArgAlaLeuSerGlnArgAsnAspProGlnThrAlaSerArgProTrpAspL
828
760 AACAGAGAGATGGGTTTGTTCATGGGTGAAGGAGCTGGTGTCTGGTGATGGAAGCTTGGAACATGCCGA
ysGlnArgAspGlyPheValMETGlyGlyGlyAlaGlyValLeuValMETGluSerLeuGluHisAlaM
897
829 TGAAACGTGGTGCTCCAATTGTAGCAGAGTATCTTGGAGGCGCTGTTAACTGCGATGCTCATCATATGA
ETLysArgGlyAlaProIleValAlaGluTyrLeuGlyGlyAlaValAsnCysAspAlaHisHisMETT
966
898 CTGATCCAAGAGCTGATGGGCTTGGTGTCTTCATGCATTGAGAGCTGCCTTGAAGATGCTGGTGTAT
hrAspProArgAlaAspGlyLeuGlyValSerSerCysIleGluSerCysLeuGluAspAlaGlyValS

FIG. 4B

967 CACCTGAGGAGGTAAATTACATCAATGCACATGCAACTTCCACACTGGCTGGTGATCTTGCTGAGATTA 1035
erProGluGluValAsnTyrIleAsnAlaHisAlaThrSerThrLeuAlaGlyAspLeuAlaGluIleA

1036 ATGCCATTAAAAAGGTATTCAAAGCACTTCAGGGATCAAAATCAATGCCACCAAGTCTATGATAGGTC 1104
snAlaIleLysLysValPheLysSerThrSerGlyIleLysIleAsnAlaThrLysSerMETIleGlyH

1105 ACTGCCCTCGGTGCAGCTGGAGGTCTTGAAGCCATTGCCACCGTGAAGGCTATCAACACGGGATGGCTGC 1173
isCysLeuGlyAlaAlaGlyGlyLeuGluAlaIleAlaThrValLysAlaIleAsnThrGlyTrpLeuH

1174 ATCCCTCTATCAACCAATTAAACCCAGAACAGCAGTGGACTTTGATACGGTCGCAACGAGAAGAAGC 1242
isProSerIleAsnGlnPheAsnProGluProAlaValAspPheAspThrValAlaAsnGluLysLysG

1243 AGCATGAGGTGAATGTTGCCATATCAAACTCGTTTGGGTTCGGTGGACATAAACTCAGTGGTCGCTTCT 1311
lnHisGluValAsnValAlaIleSerAsnSerPheGlyPheGlyGlyHisAsnSerValValAlaPheS

1312 CTGCCTTCAAAACCCCTGATTTCCCTCAGACCCCTTTAGATCCCTCTGGTCCATCTGTTAGATCACCAACCATCA 1380
erAlaPheLysPro

1381 TCTTCTTCGCAGCTTCTTGTTTCACAAGTTGAGCGCTTCTTCCTTTCAGCTTTTGTGTTCTTATTGGTC 1449

15137

FIG. 4C

16|37

1450 ATTGTTAATTTTGGCTCAACTCTTATTGGTCATTGAGGTGTAGAGAAATCCAGATTTTTGCTTCTACAATC 1518

1519 TGTGTACGGAATGTTGTATCTTTAGTTCGTTTTATGTTTGCCAAATTTTATAAAC 1573

FIG. 4D

17/37

1	AACACATTCCGCGTGGGAAAGCTGATATGATGTTGGTGGAAACGAGGCTGCCATTATTCCTATT AsnHisIleArgArgGlyGluAlaAspMETMETIleAlaGlyGlyThrGluAlaAlaIleIleProIle	69
70	GGTGGGAGGTTTTTGTGCTTGCAGGGCGCTTTCGCAGAGGAATGATGACCCCTAAACCGCTTCGAGG GlyLeuGlyGlyPheValAlaCysArgAlaLeuSerGlnArgAsnAspProLysThrAlaSerArg	138
139	CCTGGGATAAACAGAGAGATGGCTTTGTAATGGTGAAGGAGCTGGTGTTCCTGGTGATGGAAGCTTG ProTrpAspLysGlnArgAspGlyPheValMETGlyGluGlyAlaGlyValLeuValMETGluSerLeu	207
208	GAACATGCCGATGAAGCGTGGTGGCCCAATAGTAGCAGAGTATCTTGGAGGTGCTGTAACTGTGATGCT GluHisAlaMETLysArgGlyAlaProIleValAlaGluTyrLeuGlyGlyAlaValAsnCysAspAla	276
277	CATCATATGACTCAAGAGCTGACGGCTTGGTGTCTCTTCATGCATTGAGAGCTGCCCTTGAAGAT HisHisMETThrAspProArgAlaAspGlyLeuGlyValSerSerCysIleGluSerCysLeuGluAsp	345
346	GCTGGTGTTCACCCGAGGAGGTAAATTACATCAATGCGCATGCAACTTCCACACTTGCTGGTGATCTT AlaGlyValSerProGluGluValAsnTyrIleAsnAlaHisAlaThrSerThrLeuAlaGlyAspLeu	414
415	GCTGAGATTAATGCCATTAAAAAGGTATTCAAGAGCAGCTGCTGGGATCAAAATCAATGCCACCAAGTCT AlaGluIleAsnAlaIleLysLysValPheLysSerThrAlaGlyIleLysIleAsnAlaThrLysSer	483

FIG. 5A

18|37

484 ATGATAGGTCACCTGCCTCGGTGCAGCTGGAGGTCTTGAAGCCATTGCGACTGTGAAGGCTATCAACACT 552
METIleGlyHisCysLeuGlyAlaAlaGlyGlyLeuGluAlaIleAlaThrValLysAlaIleAsnThr

553 GGATGGCTTCATCCCTCAATCAACCAATTaaCCAGAACAGCCGTGGACTTTTGACACGGTCGCAAAC 621
GlyTrpLeuHisProSerIleAsnGlnPheAsnProGluProAlaValAspPheAspThrValAlaAsn

622 GAGAAGAAGCAGCATGAGGTGAACGTTGCTATATCAAAATTCGTTTGGGTTCCGGTGGACACAACTCAGTT 690
GluLysLysGlnHisGluValAsnValAlaIleSerAsnSerPheGlyPheGlyGlyHisAsnSerVal

691 GTCGCCCTTCTCTGCCCTTCAAACCCTGATTCCTTCAAGACCCTTTTGTAATTTTCTTCTCCAATATTACA 759
ValAlaPheSerAlaPheLysPro

760 TCACCACCATCATCCAGGCATCATCTTCCTTGAGCTTCTTGGTCCACGAGTTTGAGCTCTTCTTCT 828

829 TGGCGTTTACGTTCCATTCAACATTGTTCTTATTGTTTCATTGAGATTTCAAATTTTGCTTCTCAATCG 897

898 TAAGAAATGTTTGATCTGTATCTGTATCTGTAGTTCGTTTCATATTTGTCTAATTTATAACAGAACCA 966

967 ATAATCTTGTAGCAATGATGTTATTTCAGAGTTCTCAATCTT 1007

FIG. 5B

19|37

CCCCCCGACG CGTCCAAACA CTAAGTGTG AGAGAGAGAT CAGATAATCT TTCTCGTTTT 60
CTCCACCTTC ATCCGAGTAT GACGATGGGT GGTGCGTCTT TATGCGATTC ACTAGTGGCT 120
GCTTGCAATG CCTCCGCCCTC GCACTCAAGC GGAGACCGAC TGACTCAATT CATCTGGCCT 180
CGCCGGAGTA GACTGGTTAA CAACTGCTCG CTCCATGGAT CCCAGGCGAG TTCCCGTAAC 240
AACAATGCCT CGTCTTCCCT CTTCGAATCG AATAACACTT CCTTCAATCC AAAGCAGAGG 300
AGATTCAATC GAGCATCAAC CTCTGGGCAA GTCACTACAC TAGAGATGGA GAAGGACGCA 360
ATGGTAAACA AGCCACGCCG AGTTGTTGTC ACTGGCATGG GAGTTGAAAC ACCACTAGGT 420
CACGACCCCT ATACTTTTAA TGACAACTTG CTACAAGGCA AAAGTGGTAT AAGCCATATA 480
GAGAGTTTCG ACTGTTCTGC ATTTCCCACT AGAATCGCTG GGGAGATTAA ATCTTTTTCG 540
ACCGACGGAT TGGTTGCTCC TAAACTTCC AAAAGGATGG ACAAGTTCAT GCTCTACCTT 600

FIG. 6A

20137

CTAACCGCG GCAAGAAGGC GTTGGAGGAT GGTGGGGTGA CTGGGGATGT GATGGCAGAG 660
TTCGACAAAT CAAGATGTGG TGTCTTGATT GGCTCAGCAA TGGGAGGCAT GAAGGTCTTT 720
TACGATGCGC TTGAAGCTTT GAAAATCTCT TACAGGAAGA TGAACCCCTT TTGTGTACCT 780
TTTGCCACCA CAAACATGGG TTCCGCTATG CTTGCCCTTG ATCTGGGATG GATGGGTCCA 840
AACTACTCTA TTTC AACCGC ATGTGCCACG GGAAACTTCT GTATTCTCAA TGGGGCAAAC 900
CACATTACCA GAGTGAAGC TGATGTAATG CTCTGTGGTG GCTCTGACTC AGTTATTATT 960
CCAATAGGT TGGGAGGTTT TGTGCCCIGC CGGCTCTTT CAGAAAATAA TGATGATCCC 1020
ACCAAAGCTT CTCGTCCTTG GGATAGTAAC CGAGATGGTT TTGTTATGGG AGAGGGAGCC 1080
GGAGTTCTAC TTTTGAAGA ACTTGAGCAT GCCAAGAGGA GCAACTATAT ACGCAGAGTT 1140
CCTTGGGGT AGTTTCACAT GTGATGCATA CCATATAACC GAACCACGTC CTGATGGTGC 1200

FIG. 6B

21137

TGGTGTCAAT CTTGCTATCG AGAAGCGGT AGCTCATGCC GGGATTCTTA AGGAAGACAT 1260
AAATTACGTG AATGCTCATG CTACCTCTAC ACCAGCTGGA GACCTTAAGG AGTACCACGC 1320
TCTTTCTCAC TGTTTTGCC AAAATCCTGA GCTAAGAGTA AACTCAACA AATCTATGAT 1380
TGGACACTG CTGGGAGCTT CTGGGGCCGT GGAGGCTGTT GCAACCGTTC AGGCAATAAA 1440
GACAGGATGG GTTCATCCAA ATATCAACCT CGAGAATCCA GACAAAGCAG TGGATACAAA 1500
GCTTTTGGTG GGTCTTAAGA AGGAGAGACT GGATATCAA GCAGCCTTGT CAAACTCTTT 1560
CGGCTTTGGT GGCCAGAACT CTAGCATAAT TTTGCTCCT TACAAATGAA AGCGAATAG 1620
TCCAATGCTG TGTACTCTTG TGTAACCTGC TGTAAGTGTG TACAAGAACT TCCCATGTTT 1680
TGATGCAATA TGTACGAGAA CTTCCTATGC TTTTGGTAGT GCCATGATTC AGGATTCGAT 1740
TAACTTGCAC AAAGAGTTTA AGCAACGTTG AAAAGAGAGA GAAAAAATA GTGATGAGGT 1800

FIG. 6C

22|37

AGCTGAGGAT TTGTCAGGAA CAACAATACT TCATTTTCA CTTTGGTTAG GTAGACTGAA 1860

ATATTGAGC CAACATTCT TGTATTTTA TTCTTTGAAA GCTTTAACCA AAGAAAAAA 1920

AA 1922

FIG. 6D

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Met Thr Met Gly Gly Ala Ser Leu Cys Asp Ser Leu Val Ala Ala Cys
 1 5 10 15
 Met Ser Ser Ala Ser His Ser Ser Gly Asp Arg Leu Thr Gln Phe Ile
 20 25 30
 Trp Pro Arg Arg Ser Arg Leu Val Asn Asn Cys Ser Leu His Gly Ser
 35 40 45
 Gln Ala Ser Ser Arg Asn Asn Ala Ser Ser Ser Leu Phe Glu Ser
 50 55 60
 Asn Asn Thr Ser Phe Asn Pro Lys Gln Arg Arg Phe Asn Arg Ala Ser
 65 70 75 80
 Thr Ser Gly Gln Val Thr Thr Leu Glu Met Glu Lys Asp Ala Met Val
 85 90 95
 Asn Lys Pro Arg Arg Val Val Thr Gly Met Gly Val Glu Thr Pro
 100 105 110
 Leu Gly His Asp Pro His Thr Phe Tyr Asp Asn Leu Leu Gln Gly Lys
 115 120 125

FIG. 7A

24137

Ser Gly Ile Ser His Ile Glu Ser Phe Asp Cys Ser Ala Phe Pro Thr	
130	140
Arg Ile Ala Gly Glu Ile Lys Ser Phe Ser Thr Asp Gly Leu Val Ala	
145	155
150	160
Pro Lys Leu Ser Lys Arg Met Asp Lys Phe Met Leu Tyr Leu Leu Thr	
165	170
175	
Ala Gly Lys Lys Ala Leu Glu Asp Gly Gly Val Thr Gly Asp Val Met	
180	185
190	
Ala Glu Phe Asp Lys Ser Arg Cys Gly Val Leu Ile Gly Ser Ala Met	
195	200
205	
Gly Gly Met Lys Val Phe Tyr Asp Ala Leu Glu Ala Leu Lys Ile Ser	
210	215
220	
Tyr Arg Lys Met Asn Pro Phe Cys Val Pro Phe Ala Thr Thr Asn Met	
225	230
235	240

FIG. 7B

25137

Gly Ser Ala Met Leu Ala Leu Asp Leu Gly Trp Met Gly Pro Asn Tyr
 245 250 255

 Ser Ile Ser Thr Ala Cys Ala Thr Gly Asn Phe Cys Ile Leu Asn Ala
 260 265 270

 Ala Asn His Ile Thr Arg Gly Glu Ala Asp Val Met Leu Cys Gly Gly
 275 280 285

 Ser Asp Ser Val Ile Ile Pro Ile Gly Leu Gly Phe Val Ala Cys
 290 295 300

 Arg Ala Leu Ser Glu Asn Asn Asp Asp Pro Thr Lys Ala Ser Arg Pro
 305 310 315 320

 Trp Asp Ser Asn Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val
 325 330 335

 Leu Leu Leu Glu Glu Leu Glu His Ala Lys Arg
 340 345

FIG. 7C

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```

Ile Tyr Ala Glu Phe Leu Gly Gly Ser Phe Thr Cys Asp Ala Tyr His>
.1      5      10      15
Ile Thr Glu Pro Arg Pro Asp Gly Ala Gly Val Ile Leu Ala Ile Glu>
      20      25      30
Lys Ala Val Ala His Ala Gly Ile Ser Lys Glu Asp Ile Asn Tyr Val>
      35      40      45
Asn Ala His Ala Thr Ser Thr Pro Ala Gly Asp Leu Lys Glu Tyr His>
      50      55      60
Ala Leu Ser His Cys Phe Gly Gln Asn Pro Glu Leu Arg Val Asn Ser>
      65      70      75      80
Thr Lys Ser Met Ile Gly His Leu Leu Gly Ala Ser Gly Ala Val Glu>
      85      90      95
Ala Val Ala Thr Val Gln Ala Ile Lys Thr Gly Trp Val His Pro Asn>
      100     105     110

```

FIG. 8A

27137

Ile Asn Leu Glu Asn Pro Asp Lys Ala Val Asp Thr Lys Leu Leu Val>
115 120 125

Gly Leu Lys Lys Glu Arg Leu Asp Ile Lys Ala Ala Leu Ser Asn Ser>
130 135 140

Phe Gly Phe Gly Gly Gln Asn Ser Ser Ile Ile Phe Ala Pro Tyr Lys>
145 150 155 160

FIG. 8B

1 ATGATTACCTGAAAAATAAGTATAAATTTGTATTGAAATTATAAAAGTGACATTTTTTTGTGTAAACAATATT 69

70 TTGTGTACAAGAATTAAAAAATTAAGAAATATACTCAGCTTTTTTTAATAATAAAAAAATTAATTG 138

139 AGTTAGAAAAATTGTTGTACCAATAACAAAAGATTTATATGGAAATTATAAAATCAACACACCAATAACAC 207

208 AAGACTTTTTTAAAAATTTAAGAAATAATAAGCAATAACAATAGAAATCTTCAAAATTTCTCAAAATCCCTTA 276

277 AAAATCAATCTCCCACTATTAAATCCCCCTTAGTTTTAGTTGGTAATGGCAACGTTTGTGTGACTACCGTA 345

346 TTGTAACTTTTGTCAAATTGTCAATAATACGTGTCAAACTCTGGTAAAAAATTAGTCTGTGTACATCTGT 414

415 CTTTATTATATAAACACAGCTGTTAATCAGAAATTTGGTTTATTAATCAACAACCTGCACGAAACTTG 483

484 TGTGAGCATATTTTGTCTGTTTCTGTTCATGACCTTCTCCGCATGATGGCCAAGTGTAAATGGCCACT 552

28|37

FIG. 9A

BglII
 |
 553 TGCAAGAGCGTTTCTTCAACGAGATAAGTCGAACAAATATTTGTCCGTTACGACCACATATAANATCTC 621
 616
 622 CCCATCTCTATATATAATACCAGCATTCACCATCATGAATACCTCAAAATCCCAATCTCACAAATACTTC 690
 691 AATAAAAGACCAAAATAATTAAGCAAGAAAGCCTTCTTGTGCACAAAAAAGAGCCTTCT 759
 760 AGGTTTTCACGACATGAAGTTCACACTACTCTAATGGTCATCACATTGGTGATAATCGCCATCTCGTCTCC 828
 METLyspheThrThrLeuMETValIleThrLeuValIleIleAlaIleSerSerPr
 829 TGTTCCAATTAGAGCAACCAACGGTTGAAAGTTTCGGAGAAGTGGCACAAATCGTGTGTGTGACAGAACT 897
 ovalProIleArgAlaThrThrValGluSerPheGlyGluValAlaGlnSerCysvalValThrGluLe
 898 CGCCCCATGCTTACCAGCAATGACCAACGGCAGGAGACCCGACTACAGAATGCTGCGACAAACTGGTAGA 966
 uAlaProCysLeuProAlaMETThrThrAlaGlyAspProThrThrGluCysCysAspLysLeuValGI
 967 GCAGAAACCATGTCTTTGTGGTTATATTCGAAACCCAGCCTATAGTATGTATTCTCTCCAAACGG 1035
 uGlnLysProCysLeuCysGlyTyrIleArgAsnProAlaTyrSerMETTyrValThrSerProAsnGI

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FIG. 9B

1036 TCGCAAAGTCTTAGATTTTGTAAAGGTTCCCTTTCTAGTTGTTAAATCTCTCAAGACATTGCTAAGAA 1104
YArgLysValLeuAspPheCysLysValProPheProSerCys .

BglII HindII
| |
1105 AAATATTATAAAATCAAACTAGATCTGATGTAACAATGAATCATCATGTTATGGTTGAA 1173
1173 1136

1174 GCTTATATAGCTGAAGTGTTTGTGATTTTATATATGTTGTGTGTCCTGCTCAATTTTGAACAC 1242

1243 ACACGTTTCTCCTGATTTGGATTAAATTATATTTTGAGTTAAAAAGAAAGATGGAATGCTATT 1311

EcoRV
|
1312 TATACAAAGTTGATGAAAAGTGGAAGTACAATTAGATATCTCCWNCACTTAAAGAATGAAACAATAAT 1380
1350

SalI
|
1381 AGACTTCGAAACAAATGAAAAATACATAAATTGTCGACAATCAACGTCGATCGACGAGTTTATTATTAA 1449
1414

FIG. 9C

31137

1450 AAATTGTGTGAAGGACTAGCAGTTCAACCAAATGATATTGAACATATACATCAACAAATATGATAATC 1518
1519 ATAAAAGAGAGAATGGGGGGGGGTGTCGTTTACCAGAAACCTCTTTTCTCAGCTCGCTAAACCCCTA 1587
1588 CCACTAGAGACCTAGCTCTGACCGTCCGGCTCATCGGTGCCGGAGGTGTAAACCTTTCTTTCCCATGACCC 1656
1657 GAAACCTCTCTTTCCCAACTCACGAAACCCCTACAATCAAAAACCTAGCTCCGACCATCGGCTCATCGG 1725
1726 TGCCGAAGGTGTAAACCTTTCNCTCCCATCATAGTTTCTCGTAAATGAAAGCTAATTGGGCAATCGATT 1794
1789
1795 TTTAATGTTTAAACCATGCCAAGCCATTCTTTATAGGACAAATTGTCAATAATAGCATCTTTTGAGTTT 1863
1864 GTCTCAAAGTGACACTAGAAAGAAAAAGTCACAAAATGACATTCAATAAAAAAGTAAAAATATCCCTAA 1932

ClaI
|

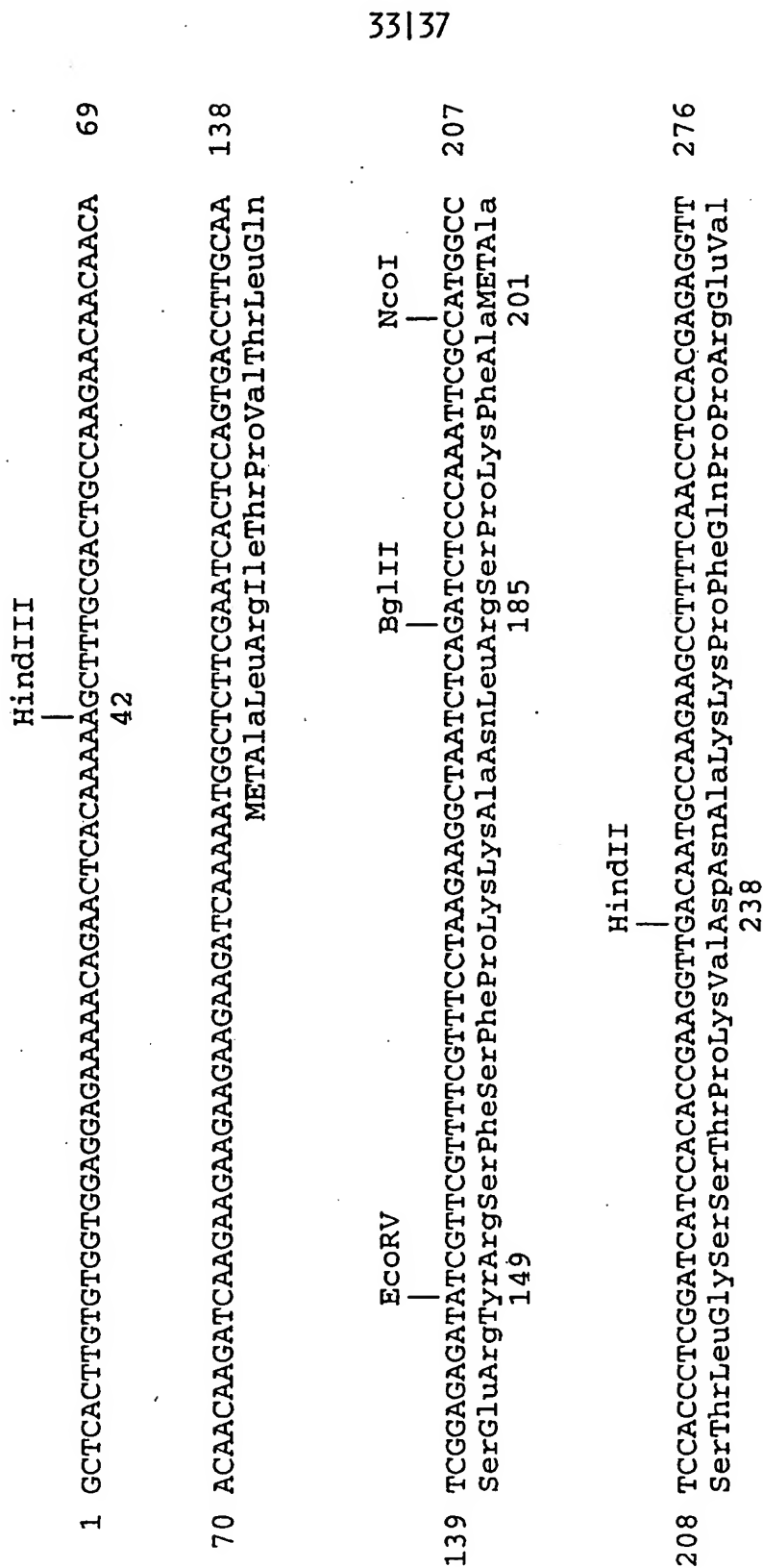
FIG. 9D

32|37

1933 TACCTTGGTTTAAATTAAATAAGTAAACAAAAATAAAATAAAACAAATATAAAATAAAAAATGA 2001

2002 AAAAAAGAAATTTTTTATAGTTTCAGATTATATGTTTTCAGATTTCGAAATTTTTTTAA 2060

FIG. 9E



33|37

FIG. 10A

34 | 37

FIG. 10B

35|37

BamHI
 691 AGGCAGATACAGAAACAATTTCAGTATCTCATTTGGGTGAGGAATGGATCCTCGTACCGAAACAGCCCC 759
 ArgGlnIleGlnLysThrIleGlnTyrLeuIleGlySerGlyMETAspProArgThrGluAsnSerPro
 736
 760 TACCTTGGGTTTCATCTACACATCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGG 828
 TyrLeuGlyPheIleTyrThrSerPheGlnGluAlaThrPheValSerHisGlyAsnThrAlaArg
 SphI
 829 CATGCAAAGGATCATGGGACGTGAAACTGGCGCAAAATTGTGTACAAATCGCGTCTGACGAAAAGCGT 897
 HisAlaLysAspHisGlyAspValLysLeuAlaGlnIleCysGlyThrIleAlaSerAspGluLysArg
 833
 ClaI
 898 CACGAGACCGCTTATACAAAAGATAGTCGAAAAGCTATTCGAGATCGATCCTGATGGCACCCTTCTTGCT 966
 HisGluThrAlaTyrThrLysIleValGluLysLeuPheGluIleAspProAspGlyThrValLeuAla
 942

FIG. 10C

BglII
 |
 967 TTTGCCGACATGATGAGGAAAAGATCTCGATGCCCGCACACTTGATGTACGATGGCGGTGATGACAAC 1035
 PheAlaAspMETMETArgLysIleSerMETProAlaHisLeuMETTyrAspGlyArgAspAsn
 990

AccI
 |
 1036 CTCCTCGAACATTTCTCGGCGGTTGCCCAAAGACTCGGCGTCTACACCGCCAAAGACTACGCCGACATA 1104
 LeuPheGluHisPheSerAlaValAlaGlnArgLeuGlyValTyrThrAlaLysAspTyrAlaAspIle
 1077

1105 CTGGAATTTCTGGTCGGCGGTGGAAGTGCGGATTTGACCGGCTATCTGGTGAAGGCGTAAAGCG 1173
 LeuGluPheLeuValGlyArgTrpLysValAlaAspLeuThrGlyLeuSerGlyGluGlyArgLysAla

SacI
 |
 1174 CAAGATTATGTTTGGGGTTCACCAAGAATCAGAAGGCTGGAGGAGAGAGCTCAAGGGCGAGCAAAG 1242
 GlnAspTyrValCysGlyLeuProProArgIleArgArgLeuGluGluArgAlaGlnGlyArgAlaLys
 1228

FIG. 10D

37|37

PvuII
|

1243 GAAGGACCTGTTGTTCCATTTCAGCTGGATTTCGATAGACAGGTGAAGCTGTGAAGAAAAAACC GA 1311
GluGlyProValValProPheSerTrpIlePheAspArgGlnValLysLeu
1266

1312 GCAGTGAGTTCGGTTTCTGTGGCTTATTGGGTAGAGGTTAAACCTATTTTAGATGTCGTTCGTGT 1380

1381 AATGTGGTTTTTTTTTCTCTAATCTGAATCTGGTATTGTGTCGTTGAGTTCGCGTGTGTGTAACCTG 1449

1450 TGTGGCTGTGGACATATTATAGAACTCGTTATGCCAATTTTGATGACGGTGGTTATCGTCTCCCCCTGGT 1518

1519 GTTTTTTTATTGTTT 1533

FIG. 10E

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/10526

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : C07H 21/04; C12N 5/00, 15/00; C12P 7/64, 21/04

US CL : 435/69.7, 69.8, 70.1, 134, 172.3, 240.4; 536/23.2, 23.4, 23.7, 24.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.7, 69.8, 70.1, 134, 172.3, 240.4; 536/23.2, 23.4, 23.7, 24.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, A, 5,110,728 (KRIDL ET AL) 05 MAY 1992, see column 1, lines 20-42; column 9, lines 51-64; column 10, lines 61-68; column 15, lines 3-55; column 16, lines 8-12 and 48-51.	1-7, 10, 17-24, 26, 33-35, 37, 39
Y	TRENDS IN BIOTECHNOLOGY, Volume 5, No. 2, issued 1987, V. C. Knauf, "The Application of Genetic Engineering to Oilseed Crops", pages 40-47, see pages 43-45.	1-7, 10, 17-24, 26, 33-35, 37, 39
Y	CARLSBERG RESEARCH COMMUNICATIONS, Volume 53, issued 1988, S. Kauppinen et al, " β -Ketoacyl-ACP Synthase I of <i>Escherichia coli</i> : Nucleotide Sequence of the <i>fabB</i> Gene and Identification of the Cerulenin Binding Residue", pages 357-370, see page 361.	1-7, 10, 17-24, 26, 33-35, 37, 39



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be part of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier documents published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"G" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

04 JANUARY 1994

Date of mailing of the international search report

07 FEB 1994

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/10526

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	THE JOURNAL OF BIOLOGICAL CHEMISTRY, Volume 267, No. 10, issued 05 April 1992, J. Tsay et al, "Isolation and Characterization of the β -Ketoacyl-acyl Carrier Protein Synthase III Gene (<i>fabH</i>) from <i>Escherichia coli</i> K-12", pages 6807-6814, see page 6810.	4, 18, 24, 35

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/10526

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
(Telephone Practice)
Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7, 10, 17-24, 26, 33-35, 37 and 39

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US93/10526

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

- I. Claims 1-7, 10, 17-24, 26, 33-35, 37 and 39, drawn to a recombinant DNA construct comprising a bacterial β -ketoacyl-ACP synthase gene, plant cells containing the construct, and a method of use, classified in Class 435, Subclass 172.3, for example.
- II. Claims 8-10, drawn to plant cells containing a DNA construct comprising a gene encoding a desaturase or a thioesterase, classified in Class 435, Subclass 240.4, for example.
- III. Claims 11-16, drawn to a DNA construct comprising a plant β -ketoacyl-ACP synthase gene and plant cells containing the construct, classified in Class 536, Subclass 23.6, for example.
- IV. Claims 25-26, 36-37 and 39, drawn to a method of using a DNA construct comprising a plant β -ketoacyl-ACP synthase gene, classified in Class 435, Subclass 240.45, for example.
- V. Claims 27-32 and 38, drawn to plant cells and plant seeds having modified fatty acid composition, classified in Class 800, Subclass 250, for example.
- VI. Claims 40-41, drawn to oil, classified in Class 426, Subclass 601, for example.

Claims 10, 26, 37 and 39 are linking claims.

The inventions are distinct from each other because each involves a technical feature not required by any of the other inventions. The invention of Group I involves a bacterial gene not required by the other groups. The invention of Group II involves two other genes not required by the other groups. The inventions of Groups III and IV require a plant gene not required by the other groups. The invention of group IV involves processes for growing plant cells under conditions for transcription and for evaluating the change in fatty acid composition, wherein such processes are not required by the invention of Group III. The invention of Group V requires whole plant regeneration processes not required by any of the other groups. Furthermore, plants-containing altered fatty acid profiles could be produced by processes other than those recited by the other groups, such as by conventional breeding procedures or by transformation with different genes. The invention of Group VI requires oil isolation techniques not required by any of the other groups. Furthermore, oil containing modified fatty acids could be obtained by processes other than those recited by the other groups, such as chemical modification of oil produced by wild type plants or isolation from modified plants produced by traditional breeding techniques. Accordingly, the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.

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